

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 18:19:52 ; Search time 8342 Seconds
(without alignments)
11300.779 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175
Sequence: 1 atgttaaacgaattatgg.....ataataaagggtggaataa 2175

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

7: gb.pl.*

8: gb.pr.*

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10: gb.sts.*

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15: em.fun.*

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17: em.fun.*

18: em.in.*

19: em.mu.*

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37: em.htg.vit.*

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40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2175	100.0	2277	1	AF022781 Neisseria
2	2175	100.0	2277	6	A98968 Sequence 1
3	2175	100.0	2277	6	BD074755 Neisseria
4	2175	100.0	5691	1	AF049349 Neisseria
5	2170.2	99.8	2537	1	AF031432 Neisseria
6	1549.8	71.3	2519	1	AF072890 Neisseria
7	1487.2	68.4	2226	1	AF123380 Neisseria
8	1487.2	68.4	2226	6	A98972 Sequence 5
9	1487.2	68.4	2226	6	BD074757 Neisseria
10	1473	67.7	9955	1	AE002504 Neisseria
11	1473	67.7	349980	6	AX044033 Sequence
12	1462.2	67.2	2262	1	AF123381 Neisseria
13	1462.2	67.2	2262	6	A98974 Sequence 7
14	1462.2	67.2	2262	6	BD074758 Neisseria
15	1454.8	66.9	326301	1	NMA622491
16	1304.8	60.0	2169	1	AF123382 Neisseria
17	1304.8	60.0	2169	6	A98970 Sequence 3
18	1304.8	60.0	2169	6	BD074756 Neisseria
19	1296.2	59.6	2124	1	AF123383 Neisseria
20	1296.2	59.6	2124	6	A98976 Sequence 9
21	1296.2	59.6	2124	6	BD074759 Neisseria
22	678.6	31.2	1000	6	AX081510 Sequence
23	678.6	31.2	1000	6	AX374691 Sequence
24	434.2	20.0	3398	1	NMLBPAG
25	218	10.0	3171	1	NMIRA
26	174.2	8.0	3300	1	NGU16260
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29	89	4.1	309266	2	AC106972
30	88.2	4.1	2139	1	AF039311
31	88.2	4.1	2139	6	BD226953
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33	87.8	4.0	146552	10	AL714007
34	87.2	4.0	240692	2	AC111246
35	87	4.0	181206	2	AC128950
36	87	4.0	215429	2	AC128300
37	87	4.0	233895	2	AC096447
38	86.6	4.0	213739	2	AC113937
39	86.2	4.0	110000	2	AC129389_1
40	86.2	4.0	226192	2	AC094426
41	86.2	4.0	314959	2	AC106099
42	85.6	3.9	173949	10	AC132100
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ALIGNMENTS

RESULT 1	AF022781	Neisseria meningitidis	2277 bp	DNA	linear	BCT 07-FEB-1998
LOCUS	AF022781	Neisseria meningitidis	complete cds.			
DEFINITION	AF022781	Neisseria meningitidis	complete cds.			
ACCESSION	AF022781	Neisseria meningitidis	GI:2843172			
VERSION	AF022781.1	Neisseria meningitidis				
KEYWORDS		Neisseria meningitidis				
SOURCE		Neisseria meningitidis				
ORGANISM		Neisseria meningitidis				
		Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
		Neisseriaceae; Neisseria.				
REFERENCE		1 (bases 1 to 2277)				
AUTHORS		Pettersson,A., Prinz,T., Umar,A., van der Biezen,J. and Tommassen,J.				

Pred. No. is the number of results predicted by chance to have a

TITLE Molecular characterization of LbpB, the second lactoferrin-binding

JOURNAL protein of Neisseria meningitidis
Mol. Microbiol. 27 (3), 599-610 (1998)
MEDLINE 98149315
PUBMED 9489671

REFERENCE 2 (bases 1 to 2277)

AUTHORS Tommassen, A., Prinz, T., Umar, A., van der Biezen, J. and

TITLE Direct Submission
Submitted (04-SEP-1997) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES Location/Qualifiers

source

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/mol_type="genomic DNA"

/strain="BNCV"

/db_xref="taxon:487"

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/gene="lbpB"

misc_binding

57..75

/note="lbpB"

/note="putative binding site"

/bound_moiety="Fur"

100..2277

/gene="lbpB"

/note="lactoferrin receptor"

/codon_start=1

/transl_table=11

/product="lactoferrin binding protein B"

/protein_id="AAC38143.1"

/db_xref="GI:2843173"

/translations="MCKPNYGGVILVLLPALLASCIIGNFGVQPVVESTPTAIPVTFKSK
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ADVDDVDVDDADADVEQLKPEVKPQFGVFGAKKDNKEVK"

ORIGIN

Query Match 100.0%; Score 2175; DB 1; Length 2277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGCGCAATTCGGCGTCAGCTGTGTTCGATCAACCGCGACCGCGTACCGGTCACT	120
Db	160	GGCGCAATTCGGCGTCAGCTGTGTTCGATCAACCGCGACCGCGTACCGGTCACT	219
QY	121	TTCAAGCTTAAGGACGTTCCCACTCGCCCTCGCCCAACCTTCTATAGAAATCACGCCG	180
Db	220	TTCAAGCTTAAGGACGTTCCCACTCGCCCTCGCCCAACCTTCTATAGAAATCACGCCG	279
QY	181	GTCAACCGCGCGCGTGGTGGCAATGCGGCTGCCAAGCGGAATACTGTTTTCAT	240
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QY	241	CGTGAAGTGGCAGCAATTCGAATAGCAACACGACGAGAAAGTGTGCTTTCAA	300
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Db	580	TGGCTTCAGATTACAAGAGTGTTCACACCGCTTAGGTATGACGGTTTGTATATATAT	639
QY	541	TCCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGGACCGTGGAAATATCTGGTAAC	600
Db	640	TCCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGGACCGTGGAAATATCTGGTAAC	699
QY	601	TGGCAATATATGACCGATGCGCAACACGTCATCGAGCAGGTAAAGCGGTGGCATTGACAAT	660
Db	700	TGGCAATATATGACCGATGCGCAACACGTCATCGAGCAGGTAAAGCGGTGGCATTGACAAT	759
QY	661	TTGGGTTATTACACATTTTATGTTAGTAAAGTGTGGTGCAACTTCTTATGCGGCTAAGGAT	720
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QY	721	GTGACGAAAGGAAACACATCTGCTTAAATATACGGTAGATTTCGGTAAACAAACCCCTG	780
Db	820	GTGACGAAAGGAAACACATCTGCTTAAATATACGGTAGATTTCGGTAAACAAACCCCTG	879
QY	781	ACGGGCGAGCTGATTAAAAACCAATATGTCAAAACCCAGTGAAGGAAACCCGCTGACC	840
Db	880	ACGGGCGAGCTGATTAAAAACCAATATGTCAAAACCCAGTGAAGGAAACCCGCTGACC	939
QY	841	ATTTAACAATCACTGCGCGATTTTAAACGGCAACCGCTTTACCGGAGTGCACAGGTCAAT	900
Db	940	ATTTAACAATCACTGCGCGATTTTAAACGGCAACCGCTTTACCGGAGTGCACAGGTCAAT	999
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Db	1060	CAGCGCTTTGAGGCGCGTTTTTTTTCGGCGATTAAGGGGAAAGAGCTTCCCGACCGTTATC	1119
QY	1021	AGCAACGACAAACGCGTATTCGGTGTATTTCGACGGCAAAACAAATAGCCCGCGCTCT	1080
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QY	1081	GGAAAAACACACCAAAATCTTGGATTCTTGAAATTTCCGTTGATGAGCAAGTGTGAA	1140
Db	1180	GGAAAAACACACCAAAATCTTGGATTCTTGAAATTTCCGTTGATGAGCAAGTGTGAA	1239
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Db	1300	GTGAGGCGCATGAAATTCCTTTGGTGTAGCAAGAAACCAATCGAGCTTCCGACGGC	1359
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Db 820 GTCCACGAAGGGAACATCTCTGCTAAATATATACGGTAGATTTTCGGTTACAAACCCCTG 879
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QY 2101 CAGTTAAACCTGAGGATTTAAACCCCAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
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RESULT 3
BD074755
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD074755
Neisseria lactoferrin-binding protein.
BD074755
2277 bp DNA linear PAT 27-AUG-2002
BD074755.1 GI:22620358
JP 2001514894-A/1.
unidentified
unclassified.
1 (bases 1 to 2277)
Fehlholm, A.M.P. and Thomsen, J.P.M.
Neisseria lactoferrin-binding protein
Patent: JP 2001514894 A 1 18-SEP-2001;
UNIVERSITY OF UTRICHT TECHNOLOGY FOUNDATION
OS Unidentified
PN JP 2001514894-A/1
PD 18-SEP-2001
PF 10-AUG-1998 JP 2000509840
PR 15-AUG-1997 GB 9717423 9,05-FEB-1998 GB 9802544.8 PI
ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA PI
THOMSEN
PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,
C07K16/12,
PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC
C12N15/00
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CC Topology: Linear;
CC Neisseria lactoferrin-binding protein
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/organism='unidentified'
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/db_xref='taxon:32644'

ORIGIN
Query Match 100.0%; Score 2175; DB 6; Length 2277;
Best Local Similarity 100.0%; Fred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTAACCGAATTATGGCGGCAATTCCTGTTGGCCCTTACTTTTGGCATCTGTATC 60
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QY 160 GCGGCAATTTCCGGCTGCGGCTGCTGTCGAATCAACGCGCGACCGCGTACCCCGTCACT 219
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QY 400 GAAAGTGTATGTTCTGTTTATACCGTTTCAAAAGGAAATTAACCTTCAACAACTTAAAGC 459
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QY 1120 AGCAACGACACACGCTATTCGTTGTTATTCGAGGCAACAAATAGCCCCCGTCCGTCT 1179
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RESULT 5

AF031432

LOCUS

DEFINITION

Neisseria meningitidis

precursor (lbpB) gene, complete cds.

ACCESSION

AF031432

VERSION

AF031432.1

GI:3213214

KEYWORDS

Neisseria meningitidis

ORGANISM

2537 bp DNA linear BCT 12-JUN-1998
B16B6 lactoferrin binding protein B

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 1 (bases 1 to 2537)
 Bonnah, R.A. and Schryvers, A.B.
 Preparation and characterization of *Neisseria meningitidis* mutants
 deficient in production of the human lactoferrin-binding proteins
 LbpA and LbpB
 J. Bacteriol. 180 (12), 3080-3090 (1998)
 98292739
 MEDLINE
 PUBMED
 9620956
 REFERENCE
 2 (bases 1 to 2537)
 Bonnah, R.A. and Schryvers, A.B.
 Direct Submission
 Submitted (24-OCT-1997) Microbiology & Infectious Diseases,
 University of Calgary, 3330-Hospital Drive N.W., Calgary, AB T2N
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FEATURES

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DEFINITION Neisseria gonorrhoeae lactoferrin binding protein B precursor (lbpB) gene, complete cds.
ACCESSION AF072890
VERSION AF072890.1 GI:4106392
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2519)
AUTHORS Biswas,G.D., Anderson,J.E., Chen,C.J., Cornelissen,C.N. and Sparling,P.F.
TITLE Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product
JOURNAL Infect. Immun. 67 (1), 455-459 (1999)
MEDLINE 99081783
PUBMED 9864256
REFERENCE 2 (bases 1 to 2519)
AUTHORS Biswas,G.D., Anderson,J.E., Cornelissen,C.N. and Sparling,P.F.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521 Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
FEATURES
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QY
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RESULT 11
AX044033/c
LOCUS
DEFINITION Sequence 112 from Patent WO0066791.
ACCESSION AX044033
VERSION AX044033.1 GI:11342917
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
Maignani, V., Galeotti, C., Mofa, M., Ratti, G., Scarselli, M.,
Scarlati, V., Rappelli, R., Frazer, C. M., and Grandi, G.
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 172 09-NOV-2000.
JOURNAL
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
Location/Qualifiers
1..349980
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/mol_type="unassigned DNA"
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Best Local Similarity 81.9%; Pred. No. 2.9e-290;
Matches 1835; Conservative 0; Mismatches 310; Indels 96; Gaps 8;
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QY	421	TATGATTATAAATTTGTPAGATCAGGTTATGTATGTATAAGGAAAG-----AT	471
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Db	97756	GAGCGGCTATCGGCAACCCATTCATGGGCAATCATCGCGATTAAGAGCGGCAAAA	97697
QY	1735	GCAATATTTACCGTTGATTTTCGGCAAGAAATCGATTTCCGGAACGCTGACGGAGAAAAC	1794
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RESULT 12			
AF123381			
LOCUS			
DEFINITION			
Neisseria meningitidis strain m990 lactoferrin-binding protein			
precursor (lbpB) gene, complete cds.			
ACCESSION			
AF123381			
VERSION			
AF123381.1			
KEYWORDS			
GI:4884688			
SOURCE			
ORGANISM			
Neisseria meningitidis			
Neisseria meningitidis			
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
Neisseriaceae; Neisseria.			
REFERENCE			
1 (bases 1 to 2262)			
AUTHORS			
Petterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.			

Sequence variability of the meningococcal lactoferrin-binding protein lbpB

Gene 231 (1-2), 105-110. (1999)

99250255

10231574

REFERENCE

2 (bases 1 to 2262)

Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.

Direct Submission

Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands

Location/Qualifiers

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ORIGIN

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DEFINITION Neisseria lactoferrin-binding protein.
ACCESSION BD074758
VERSION BD074758.1 GI:22620361
KEYWORDS JP 2001514894-A/4.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Felinholm,A.M.P. and Thomsen,J.P.M.
TITLE Neisseria lactoferrin-binding protein
JOURNAL Patent: JP 2001514894-A 4 18-SEP-2001;
UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION
COMMENT OS Unidentified
PN JP 2001514894-A/4
PD 18-SEP-2001
PF 10-AUG-1998 JP 2000009840
PR 15-AUG-1997 GB 9717423 9,05-FEB-1998 GB 9802544.8 PI
ANICA MARGARETA PETERSON FELINHOLM,JOHANNES PETRUS MARIA
THOMSEN
PC C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/32,C07K14/22,
C07K16/12,
PC C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68, PC
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ORIGIN

Query Match 67.2%; Score 1462.2; DB 6; Length 2262;
Best Local Similarity 81.1%; Pred. No. 3.4e-288;
Matches 1832; Conservative 0; Mismatches 343; Indels 84; Gaps 8;

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LOCUS Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 6/7.
ACCESSION AL162757 AL157959
VERSION AL162757.2 GI:7380371
KEYWORDS
SOURCE Neisseria meningitidis Z2491
ORGANISM Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 326301)
AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., DeWitt,K., Feltwell,T., Hamlin,N.,
Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,
Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
Skelton,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
JOURNAL Nature 404 (6777), 502-506 (2000)
MEDLINE 20222556
PubMed 10761919
REFERENCE 2 (bases 1 to 326301)
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1BA E-mail: parkhill@sanger.ac.uk
COMMENT Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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Job time : 8360 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 2175

Sequence: 1 atgtgtaaacgaattatgg.....ataataaagaggaggaaaaa 2175

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1980s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2175	100.0	2277	2	AAx23319 N. mening
2	1487.2	68.4	2226	2	AAx23321 N. mening
3	1473	67.7	110000	3	Continuation (2 of
4	1473	67.7	349980	3	AAf21611 Neisseria
5	1462.2	67.2	2262	2	AAx23322 N. mening
6	1454.8	66.9	2226	7	ACA41945 Prokaryot
7	1304.8	60.0	2169	2	AAx23320 N. mening
8	1296.2	59.6	2124	2	AAx23323 N. mening
9	1010.4	46.5	14652	3	AAa81482 N. mening
10	678.6	31.2	1000	4	AAf91389 N. mening
11	678.6	31.2	1000	6	ABk37769 DNA seque
12	460.4	21.2	707	3	AAa81815 N. mening
13	174.2	8.0	3300	6	ABs67377 Neisseria
14	88.2	4.1	2139	2	AAz31947 M. catarr
15	81.2	3.7	801	5	AAa81482 N. mening
16	80.8	3.7	510	5	AAa81482 N. mening
17	80.8	3.7	510	5	AAa81482 N. mening
18	80.8	3.7	510	5	AAa81482 N. mening
19	79.4	3.7	54786	8	ADA02705 Mouse zfh
20	79.4	3.7	54786	9	ADB72443 Mouse zfh
21	79	3.6	379	5	AAa81482 N. mening
22	79	3.6	379	5	AAa81482 N. mening
23	79	3.6	379	9	ADa09716 Novel DNA

24	79	3.6	2114	2	AAf11242
25	78	3.6	248	5	AAa81482
26	78	3.6	305	4	AAi21797
27	78	3.6	305	4	ABa66871 Human
28	78	3.6	305	4	ABa66871 Human
29	78	3.6	305	4	ABa66871 Human
30	78	3.6	305	4	ABa66871 Human
31	78	3.6	305	4	ABa66871 Human
32	78	3.6	305	4	ABa66871 Human
33	78	3.6	305	4	ABa66871 Human
34	78	3.6	305	4	ABa66871 Human
35	78	3.6	305	4	ABa66871 Human
36	78	3.6	305	4	ABa66871 Human
37	78	3.6	305	4	ABa66871 Human
38	78	3.6	305	4	ABa66871 Human
39	78	3.6	305	4	ABa66871 Human
40	78	3.6	305	4	ABa66871 Human
41	78	3.6	305	4	ABa66871 Human
42	78	3.6	305	4	ABa66871 Human
43	78	3.6	305	4	ABa66871 Human
44	78	3.6	305	4	ABa66871 Human
45	78	3.6	305	4	ABa66871 Human

ALIGNMENTS

RESULT 1

AAx23319
ID AAx23319 standard; cDNA; 2277 BP.
XX
AC AAx23319;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain BNCV LbpB cDNA.
XX
LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT CDS 100..2277
FT /*tag= a
FT /*product= "LbpB"
XX
PN WO9909176-A1.
XX
PD 25-FEB-1999.
XX
PF 10-AUG-1998; 98WO-EP005117.
XX
PR 15-AUG-1997; 97GB-00017423.
XX
PR 05-FEB-1998; 98GB-00002544.
XX
(UUYT-) RIJKSUNIV UTRECHT.
XX
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESRICHTING ST.
XX
Petersson-Fernholm AM, Tomassen JPM;
XX
WPI: 1999-190165/16.
XX
P-PSDB; AA93492.

New lactoferrin-binding protein B polynucleotides - obtained from
Neisseria meningitidis, used to develop products for the diagnosis,
prevention and treatment of neisserial disease, e.g. meningitis.

Claim 2; Page 74-78; 116pp; English.

This invention describes novel lactoferrin-binding protein B (LbpB)
strains of Neisseria meningitidis. The products of this invention can be
used for vaccinating humans against neisserial disease e.g. meningitis.


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QY 1099 TTGGATTCTCTGAAATTTTCGGTTGATGAGCGAAGTGTGAAAATCCCGACCGTTTGCC 1158
Db 1141 TTGGATTCTCTGAAATTTTCGGTTGATGAGCGAAGTGTGAAAATCCCGACCGTTTGCC 1200

QY 1159 ATTCTCTATGCCCGATTTTGGTTCATCCCGACAAACTTCTTGTGGAAGGCGATGAATT 1218
Db 1201 ATTTCCCTCTGCCCGATTTTGGCCATCCCGACAAACTCTCTTGTGGAAGGCGTGAATT 1260

QY 1219 CTTTGGTTAGCAAGAAACCATCGAGCTTTCGACCGCAGGAAATGACCGTCAGT 1278
Db 1261 CTTTGGTTAGCAAGAAACCATCGAGCTTTCGACCGCAGGAAATGACCGTCAGT 1320

QY 1279 GCTTGTTCGACTTTTGTGACTATGTGAACCTCGACCGGTAAACCCGAAACCGCCGCC 1338
Db 1321 GCTTGTTCGACTTTTGTGACTATGTGAACCTCGACCGGTAAACCTGACCGCCAGCA 1380

QY 1339 GCCAAACCGAAGC-----GCAGACGAAGAGATTTCGCACATGTAATGGC 1386
Db 1381 AGTAAACCAAGCGGAAGATAAAGGGAAGGATGAAGAGGATACAGCGTTGGTAAACGAC 1440

QY 1387 GAAGAAAGC---GAAGACGAATTCGGGATGAAGAAAGACCGCAGGATGACGCGCA 1443
Db 1441 GAAGAGCGACGGAAGATGAAGCGCGAAGAGCGAAGGCGGAGACGAAATCGGC 1500

QY 1444 GGAAGATGAAGCGCAGGAAGACGAAGCCACAGAAACCAAGACCGCGGAAGAGCAAA 1503
Db 1501 GATGAAGGAGGAGTTCGGAAGACGAAGCCGACAGAAACCAAGGCGCGGAAGAGCAA 1560

QY 1504 GCTGAAGAACCT-----GAAGAAAGATCGTTCGCGAAGGCAAC---GGAGTTCA 1551
Db 1561 GCTGAAGAACCTGAAGAACCGGAAGAAAGAAATCGCGCGAAGGCGCGTGTGGTTCA 1620

QY 1552 AAGCCATCTGCTGTCGCGAAGCCTTAAGGCGAGGATACGACCTTTCCTGAAA 1611
Db 1621 GACGGCATCTGCCCGCTCGGAAGCTCTTAAGGCGAGGATATCGACCTTTTCCTGAAA 1680

QY 1612 GGTATCGGACGCGCAAGAAACGAATATTCGCAAACTGGAGAAGCACGCTATACCGGCACT 1671
Db 1681 GGTATCGGACGCGGAGACCGGACATTCGCAAACTGGAGAAGCACGCTATACCGGCACT 1740

QY 1672 TGGGAAGCGGTATCGGCAAAACCCATTCATGGGAACAATCATCGGATAAAGAGCGCA 1731
Db 1741 TGGGAAGCGGTATACGCAAAACCCATTCATGGGAACAATCATCGGATAAAGAGCGCA 1800

QY 1732 AAAGCAGTATTTACCGTTGATTTTCGCAAGAAATCGATTTCCGGAACGCTGACGGAGAA 1791
Db 1801 AAAGCAGATTTGACGTTGATTTTCGCGGAAGAAATCGATTTCCGGAACGCTGACGGAGAA 1860

QY 1792 AACGGTGAACCTGCTTTCCGTATTTGAAACCGGCGTGATTTGAGGCGCAACGTTTCCAT 1851
Db 1861 AACGGTGAACCTGCTTTCCGTATTTGAAACCGGCGTGATTTGAGGCGCAATGTTTCCAT 1920

QY 1852 GCGACAGCGGCACTCGGATGACGCGATCGACCTTCGCGGCGAGGTTTCGACCAACCG 1911
Db 1921 GCGACAGCGGCACTCGGATGACGCGATCGACCTTCGCGGCGAGGTTTCGACCAACCG 1980

QY 1912 CAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGGATTTTACGCCCGAGGCGGAG 1971
Db 1981 CCAAGTTTCAAGCCAAATATCTTCTGTGAAGCGGCTTTTACGCCCGAGGCGGAG 2040

QY 1972 GAATTGGCGGTATATTTTCAATAATGATGGAAATCTCTGTTGTAATCTGAAGTACT 2031
Db 2041 GAATTGGCGGTACTATTTTCAATAATGATGGAAATCTCTGTTGTAATCTGAAGTACT 2100

QY 2032 GAAATTAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2091
Db 2101 GAAATTAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2141

QY 2092 GATGTTGAACAGTTAAACCTGAAGTTAAACCCCAATTCGGCGTGGTATTTCGGTGGAG 2151
Db 2142 --TGGCGACAGTTAAACCTGAAGCTAAACCCCAATTCGGCGTGGTATTTCGGTGGAG 2199
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QY 2152 AAAGATAATAAGAGGTGGAATA 2175
Db 2200 AAAGATAATAAGAGGTGGAATA 2223

RESULT 3
AA81489 1/c
WP Sequence split into 9 fragments LOCUS AA81489 Accession AA81489
WP Fragment Name Begin End
WP AA81489_0 1 110000
WP AA81489_1 100001 210000
WP AA81489_2 200001 310000
WP AA81489_3 300001 410000
WP AA81489_4 400001 510000
WP AA81489_5 500001 610000
WP AA81489_6 600001 710000
WP AA81489_7 700001 810000
WP AA81489_8 800001 837096

Query Match 67.7%; Score 1473; DB 3; Length 110000;
Best Local Similarity 81.9%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 310; Indels 96; Gaps 8;

QY 1 ATGTGTAACCGGAATTATGCGGCATTTGCTTGTGCCCCTTACTTTTGGCATCTTGATC 60
Db 64252 ATGTGTAACCGGAATTATGCGGCATTTGCTTGTGCCCCTTACTTTTGGCATCTTGATC 64193

QY 61 GCGGCAATTTCCGCGTGCAGCCTGTTGTCGAATCAACGCGCACCGGTTACCCGTCCT 120
Db 64192 GCGGCAATTTCCGCGTGCAGCCTGTTGTCGAATCAACGCGCACCGGTTACCCGTCCT 64133

QY 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTTCCCAACCTTCTATAGAAATCAACGCG 180
Db 64132 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTTCCCAACCTTCTATAGAAATCAACGCG 64073

QY 181 GTCAACGCGCCCGCTCGGTGCGCAATCGCGCTGCCAAGCGGGAATCTGTTTTTCAT 240
Db 64072 GTCAACGCGCCCGCTCGGTGCGCAATCGCGCTGCCAAGCGGGAATCTGTTTTTCAT 64013

QY 241 CGTGAAGATGCGACGGAATTTCCAAATAGCAAAACAGCAAGAAAGCTGTGTTTTCAA 300
Db 64012 AAACAAGACGATACGGAATTTCCCAAGCATCAGCAGAGGAGCATCTGCCGCTTAAA 63953

QY 301 GRAGGTGATCTCTGTTTGTATACGTTTCAAAAGGAATAAATCTCAACACTTAAAGC 360
Db 63952 GAGAAGATATCTGTTTTTAGACGGTACGCTGAAAGAACAGGCTGACAACTTAAAG 63893

QY 361 GAAATTCATAAAGCTGATTCCGATGTAGAAATTAGGACATCAGAAAAGGAAAAATAAAA 420
Db 63892 AAATCAACGAACGGTATTCTGATGTAGGGTTTATCACATCGAAAAGAGAGAAAA 63833

QY 421 TATGATTTAAATTTGTAGATGACGTTATGATATATGTAAGGAAAG-----AT 471
Db 63832 TATCAATATCAATTTTGTGCGGTATGTTTACAGGGCGGAAGGAGGATAAT 63773

QY 472 GAAATTAAGTGAAGTTCAGATTACAAGAGTTTTCACACCGCTTAGTTATGACGGTTTT 531
Db 63772 GAAAAAGAAAGACTTCTGATGTAAGGATTTGTTAAACGATTTAGTTATGACGGTTTT 63713

QY 532 GTATATTTTCCGGAAGCTCTTCCCAATCTTTTACCGAGTGCAGGACCGGTGGAATAT 591
Db 63712 GTATATTTTCCGGAAGCTCTTCCCAATCTTTTACCGAGTGCAGGACCGGTGGAATAT 63653

QY 592 TCTGGTAACTGGCAATATATGACCGATGCAACAGTCATCGACAGGTAAAGCGGTGGC 651
Db 63652 TCCGGTAACTGGCAATATATGACCGATGCAACAGTCATCGGACAGGTAAAGCGGTTC 63593

QY 652 ATTGACAAATTTGGGTTATTACATTTTATGGTAAACGATGTTTGGTCAACTCTTTATGCG 711
Db 63592 AGTACGGATTTGGGTTATTACCAATATTAAGTAAATTTGGGCAACTCTTTATGAG 63533

QY 712 GCTAAGGATGTGCAAGAAAGGAAAAACATCTCTGCTAAATATACGGTAGATTTTCGGTAAC 771
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63532 GCTAGGATGCGGACGAGGAAAGCATCTCCGGAATATACGTTGATTTGATAAC 63473
772 AAAACCCCTGACGGCGAGCTGATTAAACCAATATGT-----CAAAACCCAGT 819
63472 AAAACCCCTGATGCGAGCTGATTAAATCAGTATGTGCAAAATAAAAGTAATCCAAAT 63413
820 GAGAGGAAAAACCGCTGACCATTTAACAATCACTGCGGATTTAAACGGCAACCGCTTT 879
63412 GAGCCCAAAAACCGCTGACCATTTACGACATTTACGCAACATTTGGACGGCAACCGCTTT 63353
880 ACCGGCAGTCCAGAGTCAATCTCTGATTAGCGAAAGCCCATGCCAATPAAGGACATTG 939
63352 ACCGGCAGTCCAGAGTCAATCTCTGATTAGCGAAAGCCCATGCCAATPAAGGACATTG 63293
940 TTTTTCATGCGCGATGCGGCTTACGAGCTTACGAGGCGGTTTTTTCGGCGATAAGGGGAA 999
63292 TTTTTCATGCGGATGCGGCTTACGAGCTTACGAGGCGGTTTTTTCGGCGATAAGGGGAA 63233
1000 GAGCTTGGCGGAGGTTTATCAGCAACGACACAGCGTATTCGCTGATTCGCGAGGAAA 1059
63232 GAGCTTGGCGGAGGTTTATCAGCAACGACACAGCGTATTCGCTGATTCGCGAGGAAA 63173
1060 CAAAAA-----GCCCCGTCGCGCTCTGGAAAAAC 1089
63172 CAAAAACAGACAGACAGAAACGACGACATACAAACCTGCCCTCTGCTGGAAAAAC 63113
1090 ACCAAATCTTGGATTCTCTGAAAAATTCGCTGATGAGGCAAGTGTGAAATCCCCGA 1149
63112 ACCAAATCTTGGATTCTCTGAAAAATTCGCTGATGAGGCAAGTGTGAAATCCCCGA 63053
1150 CCGTTTGGCATTTCTCTATGCGCGATTTGCTGATCCGACAAATCTTGTGCAAGG 1209
63052 GAGTTTGGCATTTCTCTATGCGCGATTTGCTGATCCGACAAATCTTGTGCAAGG 62993
1210 CATGAAATCTTCTGTTAGCAAGCAAGAAACCATTCGAGCTTCCGACGGCAGGAAATG 1269
62992 CGTGAATCTTCTGTTAGCAAGCAAGAAACCATTCGAGCTTCCGACGGCAGGAAATG 62933
1270 ACCGTTCAGTCTGTTGCGACCTTTTTCGACCTATGTGAACTCGGACGGATAAAACCGAA 1329
62932 ACATTCGAACTCTGCTGCGATTTCTGACCTATGTGAACTCGGACGGATAAAACCGAA 62873
1330 CGCCCGCGCGCAACCGAAGCGGACGACGAG-----GATTCGACATT 1377
62872 CGTCCCGCGCGCAACCGAAGCGGACGACGAG-----GATTCGACATT 62813
1378 GATATGCGGAGAGAGCAAGCAAGCAATCGCGATGAAAGAGAGGCAACCGAATGCA 1437
62812 GATAGCTGGAAGAGGCGAGACGAAATCGAGAT---GAGAGGCGACCGAGACGCA 62756
1438 GCGCAGGAGATGAAGGCGAGGAGAGACGAGCCACGAAAGCAAGACGGCGAGAA 1497
62755 GCGGTAAGAGAGGAGGCGAGGAGAGAGAGCGAGCGGTAGAA-----GCTGAA 62708
1498 GACGAGCTGAAGAACCTGAAGAGATCTGCTG---GCGAGGCGAACGCGAGTTCAAC 1554
62707 GATGAGCTGAAGAACCTGAAGAGATCTGCTG---GCGAGGCGAACGCGAGTTCAAC 62648
1555 GCGATCTGCTGCTCCGGAAGCTCTAAGGCGAGGATGACCTTTTCTGGAAGGT 1614
62647 GCGATCTGCTGCTCCGGAAGCTCTAAGGCGAGGATGACCTTTTCTGGAAGGT 62588
1615 ATCCGACGCGAGAAACGATATTCGCAAACTGAGAGACGCTATACCGGCACTTG 1674
62587 ATCCGACGCGAGAAACGATATTCGCAAACTGAGAGACGCTATACCGGCACTTG 62528
1675 GAAGCGGATTCGCGAAACCCATTCAATGGGCAATCATGCGGATTAAGAGCGGCAAA 1734
62527 GAAGCGGATTCGCGAAACCCATTCAATGGGCAATCATGCGGATTAAGAGCGGCAAA 62468
1735 GCGATTTTACCGTTGATTCGCGCAAGATTCGATTCGCGGACGCTGACGGAAGAAAC 1794

62467 GCAGTATTTACCGTTGATTTTCGCGCAAGAAATCCGATTTCCGGAACGCTGACGAGGAAAC 62408
1795 GGTGTAGAACTGCTTTTCGCTGATTTGAAACGCGCTGATTCGAGGCAACGGTTTCCATGCG 1854
62407 GGTGTAGAACTGCTTTTCGCTGATTTGAAACGCGCTGATTCGAGGCAACGGTTTTCATGCG 62348
1855 ACAGCGCGCTCTCCGGATGACGGCATCGACCTTTCCGGGCGAGGTTTCGACCAAAACCGAG 1914
62347 ACAGCGCGCTCTCCGGATGACGGCATCGACCTTTCCGGGCGAGGTTTCGACCAAAACCGAG 62288
1915 ATCTTCAAGCTAATGATCTTCGCTGATGAGAGAGATTTTACGGCCCGAGCGGAGGAA 1974
62287 ACCTTCAAGCTAATGATCTTCGCTGATGAGAGAGATTTTACGGCCCGAGCGGAGGAA 62228
1975 TTGGCGGCTATTTTCAATAATGATGAGGAAATCTCTGCTGATACTGAAGTACTGAA 2034
62227 TTGGCGGCTATTTTCAATAATGATGAGGAAATCTCTGCTGATACTGAAGTACTGAA 62168
2035 AATAAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 62123
62167 AATAAAGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2094
2095 GTTGAACAGTTAAACCTGAACTTAAACCCCAATTCGCGCTGCTGATTCGTTGCGAGGAA 2154
62122 GCGAAACAGTTAGATCTGAACTTAAACCCCAATTCGCGCTGCTGATTCGTTGCGAGGAA 62063
2155 GATATAAAGAGGTCGAAAA 2175
62062 GATATGCGAGGAGTGGAAAA 62042

RESULT 4
AAF21611/c
ID AAF21611 standard; DNA; 349980 BP.
XX
AC AAF21611;
XX
DT 13-MAR-2001 (first entry)
XX
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX ds.
XX Neisseria meningitidis.
XX WO2000066791-A1.
XX PD 09-NOV-2000.
XX PF 08-MAR-2000; 2000WO-US005948.
XX PR 30-APR-1999; 99US-0132068P.
PR 08-OCT-1999; 99WO-US023573.
PR 28-FEB-2000; 2000GB-00004695.
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M., Hickey E., Peterson J., Tettelin H., Venter JC;
PI Masignani V., Galeotti C., Mora M., Ratti G., Scarselli M., Scarlato V;
PI Rappuoli R., Frazer CM., Grandi G;
XX WPI; 2000-647603/62.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
frames are used to detect, treat and prevent Neisserial infections.
XX
XX Claim 7; Appendix A; 692pp; English.
XX
CC The present invention describes the full length genome of Neisseria
meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613

not pub

CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 4980 bp
 CC (i.e. the last 4980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 4980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used
 XX
 SQ Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;

Query Match 67.7%; Score 1473; DB 3; Length 349980;
 Best Local Similarity 81.3%; Pred. No. 0;
 Matches 1835; Conservative 0; Mismatches 310; Indels 96; Gaps 8;

QY 1 ATGTGTAACCGGAATATGCGGCATGTCTTGTCGCCCTTACTTTGGCATCTTGATC 60
 DB 99481 ATGTGTAACCGGAATATGCGGCATGTCTTGTCGCCCTTACTTTGGCATCTTGATC 99422

QY 61 GCGGGCAATTCGGGTGAGCTGTGTGCGAATCAACGCGCAGCGGTACCCCGTCACT 120
 DB 99421 GCGGGCAATTCGGGTGAGCTGTGTGCGAATCAACGCGCAGCGGTACCCCGTCACT 99362

QY 121 TTCAAAGTCTAAGACGTTCCCATCTCCGCCGCCCTCCCAAACCTTCTATAGAAATCAAGCCG 180
 DB 99361 TTCAAATCTAAGACGTTCCCATCTCCGCCGCCCTCCCAAACCTTCTATAGAAATCAAGCCG 99302

QY 181 GTCAACCGGCCCGCCCGTGGTGGCAATGCGGCTGCAAGCGGGAATCTGCTTTTCAT 240
 DB 99301 GTCAACCGGCCCGCCCGTGGTGGCAATGCGGCTGCAAGCGGGAATCTGCTTTTCAT 99242

QY 241 CGTGAAGATGGCAGAAATTCAAATAGCAACCAAGCAGAGAAAGCTGTGCTTCAA 300
 DB 99241 AAACAGAGCGGTACGGAAATTCGCCAAGCATCAGGCGAGAGGAGCATCTGCCGCTTAA 99182

QY 301 GAAGGTGATGTTCTGTTTATACGTTTCAAAGGAAATAAATCTCAACAACTTAAAGC 360
 DB 99181 GAGAGGATATCTGTTTATAGCGTACGCTGAAGAACAGGCTGACAACTTAAAG 99122

QY 361 GAAATTCATAAACGATGATTCGATGTAGAAATTAGGACATCAGAAAGGAAATAAAAA 420
 DB 99121 AAAATCAACGAAACGGTATCTGATGTGAGGGTTATCACATCGAAAGAAAGAGAA 99062

QY 421 TATGATTATAATTTCTAGATCGAGTTATGTATATGTAAAGGAAAG-----AT 471
 DB 99061 TATCAATATCAATTTGTCGTCGGGCTATGTGTTTACAGGCGGGAAGGAAAGATAAT 99002

QY 472 GAAATTAAGTGACTTCAGATTACAGCAGTTTTCACACCGCTTAGGTTATGACGCTTTT 531
 DB 99001 GAAAGAAGAAAGACTTCTGATGTAAGAGTTTGTGTTAAACCGATTAGTTATGACGCTTTT 98942

QY 532 GTATATATTCGGGAAGCTCTTCCCAATCTTTACCGAGTCCGGGAACGGTGAATAT 591
 DB 98941 GTATATATTCGGGAAGCTCTTCCCAATCTTTACCGAGTCCGGGAACGGTGAATAT 98882

QY 592 TCTGTTAACTGCAATATATGACCATGCGCAACGTCATCGAGCAGGTAAGCGGTGCG 651
 DB 98881 TCCGGTAACTGCAATATATGACCATGCGCAACGTCATCGAGCAGGTAAGCGGTGCG 98822

QY 652 ATTGACAAATTTGGTATTACACATTTTATGTTAAGATGTTGGTGCACTTCTTATGCG 711
 DB 98821 ACTACGATTTGGTATTACACATTTTATGTTAAGATGTTGGTGCACTTCTTATGAG 98762

QY 712 GCTAAGGATGTGACGAAGGAAAAACATCTCTCTAAATATACGCTAGATTTCGGTAAC 771
 DB 98761 GCTAAGGATGCCGACGACAGGAAAAACATCTCTCCGAATATACGCTAGATTTCGTAAC 98702

QY 772 AAAACCTGTAGCGGCGAGCTGATTAATAAACCAATATGT-----CAAACCCAGT 819
 DB 98701 AAAACCTGATGCGCAAGCTGATTAATAATCAGTATGTGCAATAAAGTAATCCAAT 98642

QY 820 GAGAGCAAAAAACCGCTGACATTTACAAATCATCATCTCCGATTTTAAACGCAACCGCTTT 879
 DB 98641 GAGCCCAAAAAACCGCTGACATTTACGACATTAACGCAACATTTGGACGCAACCGCTTT 98582

QY 880 ACCGGCAGTCCCAAGGTCAATCTGATTTAGCGAAAGCCATGCCATTAAGGACATTTG 939
 DB 98581 ACCGGCAGTCCCAAGGTAGCACCCGAGGTGAAGACGCAACGCTGATAAAGATAATTG 98522

QY 940 TTTTTCATCCGATGCCGATCAGCGCTTTGAGGGCGGTTTTTTTCGCCGATTAAGGGGAA 999
 DB 98521 TTTTTCATACCAGTCCGATCAGCGCTTTGAGGGCGGTTTTTTTCGCCGATTAAGGGGAA 98462

QY 1000 GAGCTTCCCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGTATTCGAGGCAAA 1059
 DB 98461 GAGCTTCCCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGTATTCGAGGCAAA 98402

QY 1060 CAAAAATA-----GCCCCGTGCGCTCTGGAACAC 1089
 DB 98401 CAAAAACAGACAGCAAAAAACGACGACATACAAAACCTGCCCTGTCTGGAACAC 98342

QY 1090 ACCAAATCTTGATTTCTCTGAAAAATTTCCGTTTGATGAGCAAGTGTGAAAAATCCCCGA 1149
 DB 98341 ACCAAATCTTGATTTCTCTGAAAAATTTCCGTTTGACGAGCAAGTGTGAAAAATCCCCGT 98282

QY 1150 CCGTTTGCCATTTCTCTATGCCGATTTTGTCTCCGACAAATCTTCTGTGCAAGGG 1209
 DB 98281 GAGTTTGCCATTTCTCTATGCCGATTTTGTCTCCGACAAATCTTCTGTGCAAGGG 98222

QY 1210 CATGAAATTCCTTTGTTAGCAGAAAGAAACCATCGAGCTTCCGACGCGACGAAATG 1269
 DB 98221 CGTGAATTTCTTTTGTAAACAAAGAACAAACATCGAGTTGCCGATGTGAGAAACG 98162

QY 1270 ACCGTGAGTGTGTTTGGCATTTTGTGCTATGTGAAATCTCGGACGATTAATAACCGAA 1329
 DB 98161 ACAATCCGACCTGTGCGATTTTCTGACCTATGTGAAATCGACGCGATGCAACCGAA 98102

QY 1330 CGCCCCCGCCCAACCGGAGGCGGACGAGAG-----GATTGCGACATT 1377
 DB 98101 CGTCCCGCCCAACCGGAGGCGGACGAGAGAGGAGCGAGAGGATACAGCGGTT 98042

QY 1378 GATAATGGCGAAAGAAAGCAAGACGAAATCGCGATGAAGAGAGGACCGAAGATGCA 1437
 DB 98041 GATAGCTCGAAGAGGCGAAGCAAGATCGAGAT---GAAGAGGACCGGAGACGCA 97985

QY 1438 GCGCAGGAGATGAAGGCGCAGGAAGACGAAAGCAGAACGACAGAAACGACGCGCAAGAA 1497
 DB 97984 GCGCTAAAGACGAAAGCAGGACGAAAGACGAAAGCGCTAGAA-----GCTGAA 97937

QY 1498 GAGGAGCTGAAGACCTGAAGAGATGCTGCG---GCAAGGGCAACGCGAGTTCAAAC 1554
 DB 97936 GATGAGCTGAAGACCGCGAAGAGATCCGCGACAGAAAGAGGCGGCGGTTCCAGAC 97877

QY 1555 GCCATCTTGCCTGTCCCGGAAGCCCTCTAAAGGCGAGGATATCGACTTTTCTTGAAGGT 1614
 DB 97876 GGCATCTCTCCGCTCCGGAAGCCCTTAAGGCGAGACATCGACTTTTCTTGAAGGT 97817

QY 1615 ATCCGACGCGAAGAACGAATATCCGCAATCTGAGAACGACGCTATATACCGCACTTG 1674
 DB 97816 ATCCGACGCGAAGAACGATATTCGAAAACTGAGAGACACACTATATACCGCACTTG 97757

QY 1675 GAAGCGCTATCGCAACCCCAATTCATGGGCAATCATGCGGATTAAGAACGCGCAAA 1734
 DB 97756 GAAGCGCTATCGCAACCCCAATTCATGGGCAATCATGCGGCGATTAAGAACGCGCAAA 97697

QY 1735 GCAGTATTACCGTTGATTTCGGCAAGAAATCGATTTCGCCGAACGCTGACGGAGAAAAC 1794
 DB |||||
 QY 1795 GGTGTAGAACCTGCTTTCCGCTATTGAAACCGCGTGAATGAGGGCAACGGTTTCCATGCG 1854
 DB |||||
 QY 1855 ACAGCGGCACCTCGGGATGACGATGACCTTTCCGGCGAGGGTTGACCAACACCGCAG 1914
 DB |||||
 QY 1915 ATCTTCAAGCTAATGATCTTCGTGTAGAGGAGATTTTACGGCCCGAAGCGGAGAA 1974
 DB |||||
 QY 1975 TTGGCGCGTATTATTTTCAATAATGATGGGAAATCTCTTGTTATAACTGAAGGTACTGAA 2034
 DB |||||
 QY 2035 AATAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 2094
 DB |||||
 QY 2095 GTTGAACAGTTAAACCTGAAAGTTAAACCCCAATTCGGCGCTGTTATTCGGTGGCAAGAAA 2154
 DB |||||
 QY 2155 GATAATAAGAGGTGGAAAAA 2175
 DB |||||
 QY 2175 GATAATAAGAGGTGGAAAAA 2199
 DB |||||

RESULT 5

AX23322
 ID AAX23322 standard; cDNA; 2262 BP.
 AC AAX23322;
 DT 11-JUN-1999 (first entry)
 DE N. meningitidis strain M990 LbpB cDNA.
 KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
 KW meningitis; diagnosis; treatment; ds.
 OS Neisseria meningitidis.

Key Location/Qualifiers

CDS 1..2262

FT /*tag= a

FT /product= "LbpB"

W09090176-AA

25-FEB-1999.

10-AUG-1998; 98WO-EF005117.

15-AUG-1997; 97GB-00017423.

05-FEB-1998; 98GB-00002544.

(UYUT-) RIJKSUNIV UTRECHT.

(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

Petterson-Fernholm AM, Tommassen JPM;

WPI; 1999-190165/16.

P-PSDB; AAW93495.

New lactoferrin-binding protein B polynucleotides - obtained from

PT Neisseria meningitidis, used to develop products for the diagnosis,

PT prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 98-102; 116pp; English.
 PS This invention describes novel lactoferrin-binding protein B (lbpB)
 CC strains of Neisseria meningitidis. The products of this invention can be
 CC used for vaccinating humans against neisserial disease e.g. meningitis.
 CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The lbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides

SQ Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;

Query Match 67.2%; Score 1462.2; DB 2; Length 2262;

Best Local Similarity 81.1%; Pred. No. 0;

Matches 1832; Conservative 0; Mismatches 343; Indels 84; Gaps 8;

QY 1 ATGTGTAACCGAATTATGGCGGCAATGTCCTGTGTCCTTACTTTTGGCATCTTGTATC 60

DB 1 ATGTGTAACCGAATTATGGCGGCAATGTCCTGTGTCCTTACTTTTGGCATCTTGTATC 60

QY 61 GCGGCAATTTCCGGGTGACGCTGTTGTCGAATCAACGCCGACCGCCCAACTCTGTCA 108

DB 61 GCGGCAATTTCCGGGTGACGCTGTTGTCGAATCAACGCCGACCGCCCAACTCTGTCA 120

QY 109 TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTCCGCCCTTCCCAACCTTCTATA 168

DB 121 GATTCGAATCTTCCAACTCTCGGATAAGCTCTCCAGCTCTCTGCCGAGCTTCGGTA 180

QY 169 GAAATCACCGCGTCAACCGCCCGCTCGGTGGGCAATGCGCTCCCAAGCGGAAAT 228

DB 181 GAAATCACCGCGTCAACCGCCCGCTCGGTGGGCAATGCGCTCCCAAGCGGAAAT 240

QY 229 ACTGCTTTTCATCGTGAAGATGGCAGCGAAATTCGAATAGCAACAGCAAGCAAGAAAG 288

DB 241 ATCCCACTTTTGATAAAATGGTAATCAATTCGAATAGCAACAGCAAGCAAGAAAG 300

QY 289 CTGCTGTTTCAAGAGGTGATGTTCTGTTTTTATACGGTTTCAAAAGGAAATAAATCTCAA 348

DB 301 CTGCGCTCAAGAGAGGATATCTGTTTTTATACGGTTTCAAAAGGAAATAAATCTCAA 360

QY 349 CAACTTAAAGCGAAATTCATAAAGCTGATTCGATGAGAAATAGGACATCAGAAAG 408

DB 361 AAATCTTAAAGGAAATCAACGGACGGCATCTTAATGCACCAATACACGCTCCGATTTA 420

QY 409 GAAATAAATAATGATTAATAATTTAGATGAGGTATGATATA---TCGTAAGGAA 465

DB 421 AAAGATGATGCGTATCAATATAAATATGTCGGGCGGATATGTTTATCTAGATATGA 480

QY 466 AAAGATGAAATTAAGTGACTTCAGATTACAAGCAAGTTTTCACACCGTTAGTTATGAC 525

DB 481 ACAGATGAAATCGAACAGAACTCAGCGGTAAAGCGGTTACCCACCGTTAGTTATGAC 540

QY 526 GGTGTTGATATATTTCGGGAGAACGTCCTTCCCAATCTTTACCGAGTCGGGAAAGG 585

DB 541 GGTGTTGATATATTTCGGGAGAACGTCCTTCCCAATCTTTACCGAGTCGGGAAAGG 600

QY 586 GAAATTTCTGTAATGCGCAATATATGACCGATGCCAACAGTCATCGCAGCAGTAAGG 645

DB 601 GAAATTTCTGTAATGCGCAATATATGACCGATGCCAACAGTCATCGCAGCAGTAAGG 660

QY 646 GTTGGCATTGACAATTTGGGTTATTACACATTTTATGTTAAACGATGTTGGTCAACTTCT 705

DB 661 GTTGGCATTGACAATTTGGGTTATTACACATTTTATGTTAAACGATGTTGGTCAACTTCT 720

QY 706 TATGCGGCTAAGGATGTCGACGAAAGGAAACATCTCTGCTAAATATACGCTAGATTC 765

DB 721 TATGCGGCTAAGGATGTCGACGAAAGGAAACATCTCTGCTAAATATACGCTAGATTC 780

QY 766 GGTAAACAAACCTGACGGCGGAGCTGATTAACCAACCAATATGT-----CAAACCCAGT 819

DB 781 GATAACAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 820 GAGAGCAAAACCGCTGACATTTACACATCACTCCGATTTAAACCGCAACCGCTTT 879
Db |||||
841 GAACCCAAAACCGCTGACATTTACGACATTTACGACATTTGAGCGCAACCGCTTT 900
QY 880 ACCGCGATGCCAAGTCAATCTCTGATTTAGCGAAGCCATGCAATAGGAGCATTTG 939
Db |||||
901 ACCGCGATGCCAAGTCAATCTCTGATTTAGCGAAGCCATTTGCGCGTAATAGCGCTTG 960
QY 940 TTTTTCATCCGATCGCATCAGCGCTTTGAGCGGCTTTTTCGCGGATAGGGGGAA 999
Db |||||
961 TTTTTCATCCGATCGCATCAGCGCTTTGAGCGGCTTTTTCGCGGATAGGGGGAA 1020
QY 1000 GAGCTTCCGCGATTTTATFAGCAACGACACAGCGTATTCGCTGATTTTCGAGGCAAA 1059
Db |||||
1021 GAGCTTCCGCGATTTTATFAGCAACGACACAGCGTATTCGCGTATTTTCGAGGCAAA 1080
QY 1060 CA-----AAATAGCCCGTGCCTGCGCTGCGGATAGGGGGAA 1092
Db |||||
1081 AAACAGAGACAGAAACGCGAGAGATACAAACCTGCGCTGCGGATAGGGGGAA 1140
QY 1093 AAATCTTGATTTCTCTGAAAATTTCCGTTGATGAGGCAAGTGTGAAAATCCCGACCG 1152
Db |||||
1141 AAATCTTGATTTCTCTGAAAATTTCCGTTGATGAGGCAAGTGTGAAAATCCCGACCG 1200
QY 1153 TTTGCCATTTCTCTATGCCCGATTTTGTCTATCCCGAACAATCTTCTGTCGAGGCGCAT 1212
Db |||||
1201 TTTGCCATTTCTCTATGCCCGATTTTGTCTATCCCGAACAATCTTCTGTCGAGGCGCT 1260
QY 1213 GAAATTCCTTTGTTGATGAGGCAAGAAACCATCGAGTTGCCGAGGCAAGAAATGACC 1272
Db |||||
1261 GAAATTCCTTTGTTGATGAGGCAAGAAACCATCGAGTTGCCGAGGCAAGAAATGACC 1320
QY 1273 GTGAGTCTTGTGCGATTTTGTGCTATGTGAAACTCGGACGATATAAACCAGGACGC 1332
Db |||||
1321 GTGAGTCTTGTGCGATTTTGTGCTATGTGAAACTCGGACGATATAAACCAGGACGC 1380
QY 1333 CCGCGCGCAACCGGAGGC-----CGAGGCAAGAGGATTCGGACATGAT 1380
Db |||||
1381 CCGCGAGTAAACCAAGCGGAGGATATAAGGCGAGGATGAAGCGGTGCGAGCTTGAT 1440
QY 1381 AATGGCAAGAAAGCAAGCAAGAAATCGCGATGAGGCAAGGCAAGGATGAGGC 1440
Db |||||
1441 AAGGCAAGAAAGCAAGCAAGAAATCGCGATGAGGCAAGGCAAGGATGAGGC 1500
QY 1441 GCAGGAGATGAAGCGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1482
Db |||||
1501 TCGGAGAGGATTAATGCGGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1560
QY 1483 GAAGCGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1542
Db |||||
1561 GATGAAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
QY 1543 GGCAGTTCAACCGCATCTGCTGCTCCGAGGCTTAAAGGCGAGGATTCGACCTT 1602
Db |||||
1621 GCGGTTTACGAGCATCTGCTGCTCCGAGGCTTAAAGGCGAGGATTCGACCTT 1680
QY 1603 TTTCTGAAGGATTCGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1662
Db |||||
1681 TTTCTGAAGGATTCGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1740
QY 1663 ACCGCGATTCGAGGAGCGGATTCGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1722
Db |||||
1741 ACCGCGATTCGAGGAGCGGATTCGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1800
QY 1723 GAAGCGCAAAACGAGTATTTACCGTTGATTTTCGCAAGAAATCGATTTTCGCAAGCGTG 1782
Db |||||
1801 AAAGCGCAAAACGAGTATTTACCGTTGATTTTCGCAAGAAATCGATTTTCGCAAGCGTG 1860
QY 1783 ACGGAGAAACCGGTTAGAACTGCTTTCCGTTATGAAACCGGCGTATTCGAGGCGAAC 1842
Db |||||
1861 ACGGAGCAAAACCGGTTAGAACTGCTTTCCATTTTGAAGCGGCAAGATTCATGCGAAC 1920
QY 1843 GGTTCCTATCGACAGCGCGCATCGGATGAGCGCATCGACTTCCGCGGAGGCTTCG 1902

Db |||||
1921 GGTTCACCGGACAGCGCGCATCTCGGAGAGCGGCATCAATCTTCGGGAATGGTTTCG 1980
QY 1903 ACCAACCGGAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGGATTTTACGGCCCG 1962
Db |||||
1981 ACCGACCCAAAACATTTCCAAGCTAGTAATCTTCGTGTAGAGGAGGATTTTACGGCCCG 2040
QY 1963 AAGCGGAGGAATTCGGCGTATTTTCAATGATGCGGAATCTCTTGGTATAACT 2022
Db |||||
2041 CAGCGCGGAATTCGGCGTATTTTCAATGATGCGGAATCTCTTGGTATAACT 2100
QY 2023 GAAGGTACTGAAAATAAAGTTGAAGCTGATTTGATGTTGATGTTGATGTTGATGTTGAT 2082
Db |||||
2101 GAAATATTTGAAATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2160
QY 2083 GCTGATGCTGATGTTG---AACAGTTAAACCC---TGAAGTTAAACCCCAATTCGGCGTG 2136
Db |||||
2161 GTTGAAGCTGATGTTGCAACAGTTAGAACCTGATGAAGTTAAACACAAATTCGGCGTG 2220
QY 2137 GTATTCGGTCCGAAGAAAGATATAAAGAGGTGAAAAA 2175
Db |||||
2221 GTATTCGGTCCGAAGAAAGATATAAAGAGGTGAAAAA 2259

RESULT 6

ACA41945

ID ACA41945 standard; DNA; 2226 BP.

XX ACA41945;

AC ACA41945;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #23602.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX Neisseria meningitidis.

XX W029027781-78

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KJ, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU38075.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 29815; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 2226 BP; 701 A; 466 G; 566 G; 493 T; 0 U; 0 Other;

Query Match 66.9%; Score 1454.8; DB 7; Length 2226;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 1839; Conservative 0; Mismatches 297; Indels 126; Gaps 8;

Qy	1	ATGTGTAACCGAATTATGGGGCAATCTCTGTGTGCGCTTACTTTTGGCATCTTGATC	60
Db	1	ATGTGTAACCGAATTATGGGGCAATCTCTGTGTGCGCTTACTTTTGGCATCTTGATC	60
Qy	61	GGCGCAATTTCCGGGTGCGCTTCTGTGCAATCAACCGCGACCGCGTACCCGCTCACT	120
Db	61	GGCGCAATTTCCGGGTGCGCTTCTGTGCAATCAACCGCGACCGCGTACCCGCTCACT	120
Qy	121	TTCAAGTCTAAGGAGCTTCCCACTCCGCCCTGTCGCAACCTTCTATAGAAATCAACGCG	180
Db	121	TTCAAGTCTAAGGAGCTTCCCACTTCGCGCCCTGTCGCAACCTTCTGTTAGAAACCAACGCG	180
Qy	181	GTCAACCGCGCGCGTGGTGGCGCAATGGCGTCCCAAGCGCAAGCTGCTTTTTCAT	240
Db	181	GTCAACCGCGCGCGTGGTGGCGCAATGGCGTCCCAAGCGCAAGCTGCTTTTTCAT	240
Qy	241	CGTGAAGTGGCACGGAATTCCTAATAGCAAAACAGACAGAGAAAGCTGCTGTTTCAA	300
Db	241	CGTGAAGTGGCACGCGCAATTCCTGATAGCAAAACAGACAGAGAAAGCTGCTGTTTAA	300
Qy	301	GAAGTGATGTTCTGTTTTTATACGGTTCAAAGGAAATAAATCTTCAACACTTAAAGC	360
Db	301	GAAGTGATGTTCTGTTTTTATACGGTTCCAAAAGGATATAAATCTTCAACACTTAAAGT	360
Qy	361	GAAATTCATAACGTTGATTCGATCTAGCAATTTAGCAATCAGAAAGGAAATATAAAA	420
Db	361	AAAATTCATACGCAATCTCTAATGTAGAAATTTAGCAATCAGAAATATAAAA	420
Qy	421	TATGATTTAAATTTGTAGATCAGGTTATGTATA---TGTAAGGGAAGATGAAATTT	477
Db	421	TATGATTTAAATTTGTAGATCAGGTTATGTATACTACTAAGGGAAGATGAAATTT	480
Qy	478	AAGTGACTTCAGATTACAGAGCTTTTCCACCGCTTAGGTTATGACGGTTTTGTATAT	537
Db	481	GAGTGACTTCAAATCACAGCAGTTTACCTACCGGTTTGGTTATGACGGTTTGTATAT	540
Qy	538	TATTCGGGAGAGCTCTTCCAACTTTACCGAGTGGGGAACGGTGAATATCTCGT	597
Db	541	TATTCGGGAGAGATCTCTTCGAATCTTTACCGAGCGGGGAACGGTGAATATCTCCGC	600
Qy	598	AACTGGCAATATAGCCGATCCAACTCATCGAGCAGGTAAAGC---GGTTGCAATT	654
Db	601	AACTGGCAATATAGCCGATCCATACGTATCTGAAACAGGAAACGAGAGATCTTAGC	660

Qy	655	GACAAATTTGGTTATTACACATTTTATGGTAAACGATGTTGTTGCAACTTCTTATGCGGCT	714
Db	661	GAAGATTTGGTTATTATCGTTTATTCGGTCAAAATTCGGAGCAACTTCTTATGCTGG	720
Qy	715	AAGGATGTCGACGAAAGGAAAAACATCTCTGCTAAATATACGGTAGATTTTCGGTAACAA	774
Db	721	ACTGCCGACGACCGAGAGGAAAAACATCTCTGCCAATATACGGTAGATTTTCGGTAAGAA	780
Qy	775	ACCCTGAGGGCGAGCTGATTAATAAACCAATATGT---CAAAACCGAGTGAAGCAAAA	831
Db	781	ACTTTGACGGGTAAATTAATTTAAATAATCAGTATGTCAAAAGAAAAACCGATGAAGAAA	840
Qy	832	CCGCTGACCACTTAAACATCACTGCGGATTAAACGCAACCGCTTTTACCGCGAGTGCC	891
Db	841	CCGCTGACCACTTAAACATCACTGCGGATTAAACGCAACCGCTTTTACCGCGAGTGCC	900
Qy	892	AAGGTCAATCTGATTTTAGCGAAAAGCATGCGAATAAGGAGCAATTTGTTTTCCATGCC	951
Db	901	AAAGTTAAACCGAGGTGAAGACGAAACACGCTGATAAAGAGCAATTTGTTTTCCATACC	960
Qy	952	GATCGCGATCAGCGCTTTAGGGCGGTTTTTTTCGGCGATAGGGGGAAGAGCTTGGCCGA	1011
Db	961	GATCGCGATCAGCGCTTTAGGGCGGTTTTTTTCGGCGATAGGGGGAAGAGCTTGGCCGA	1020
Qy	1012	CGGTTTATCAGCAACGACAGCGTATTTCGGTGTATTTCGCGAGCAACAAAAATAGCCCC	1071
Db	1021	CGGTTTATCAGCAACGACAGCGTATTTCGGTGTATTTCGCGAGCAACAAAAATAGCCCC	1080
Qy	1072	G-----TGCCGCTCTGGAACACACACCAAAATCTTG	1101
Db	1081	GCATCAACCGCATCAGATACAAATCTCTGCTATGCGCTGAAACACACCAAAATCTTG	1140
Qy	1102	GATTTCTGAAAAATTTTCGTTGATGAGCAAGTGGTGAATATCCCGACCGTTTGGCAAT	1161
Db	1141	GATTTCTGAAAAATTTTCGTTGATGAGCAAGTGGTGAATATCCCGACCGTTTGGCAAT	1200
Qy	1162	TCTCCTATGCGCGATTTTGGTTCATCCCGACAACTCTTGTGCGAGGCGCATGAAATCTCT	1221
Db	1201	TCCCTATGCGCGATTTTGGTTCATCCCGACAACTCTTGTGCGAGGCGGTGAATCTCTC	1260
Qy	1222	TTGTTAGCCAAAGAAAAACCATCGAGCTTCCGACGGCAGGAAATGACCGTCTAGTCT	1281
Db	1261	TTGTTCAAGATATCTCAAAACCATCGATCTTCCGACGGCAGGAAATGACCGTCTAGTCT	1320
Qy	1282	TGTTGCGACTTTTGAACCTATGTGAACCTCGACGGGTAATAAACCGACGCGCCCGCCG	1341
Db	1321	TGTTGCGACTTTTGAACCTATGTGAACCTCGACGGGTAATAAACCGACGCGCCCGCCG	1380
Qy	1342	AAACCGAAGCGCAGGACGAAAG---GGATTTCGGACATTGATAATGGCGAAGAAAGCGAA	1398
Db	1381	AAACCGAAGCGCGAAGATGAAATTTCCGAGATGAAATTTGGTGAAGCGGAAATGAA	1440
Qy	1399	GACGAAATTCGGCGATGAAGAAAGGACCGAAGATGACCGCGCAGGAGATGAAGCGCAGC	1458
Db	1441	GAGGATTTGCTCGCTGAAGAAAGAAACACGGAAGACGAAAGTCTGTAGAGATGAAGACAG	1500
Qy	1459	GAAGAAGCGAAGCCACAGAAAAAC-----	1482
Db	1501	GAAGAAGCGAAGTTTCCGAAAGATGGTAAACAGTGAAGACGAAAGAAATCCCGAAGAA	1560
Qy	1483	-----GAAGACGGCGAAGAAACGAACTGAAGAACTGAAGAAATTCGTCGCGAGAA	1536
Db	1561	GATGATGATGAAGCGAAGAGAGGAAGTTGAAGAACCGGAAAGAAATTCGCGCGAAGAA	1620
Qy	1537	GGCAAC---GGCAGTTCAAACGCCATCTCTGCTGTCGCGAAGCCTCTAAAGGCGAGGAT	1593
Db	1621	GGCGCGGTGGCGGTTTCAGACGGCATCCCGCCGCTTCGGAAGCCCTTAAAGCGAGGAC	1680
Qy	1594	ATCGACCTTTCTCTGAAAGGTTATTCGCGCGGAGAAACGAAATATTCGCGAAATCTGGAGA	1653
Db	1681	ATCGACCTTTCTCTGAAAGGTTATTCGCGCGGAGAAACGCAATTCGCGAAATCTGGAAAA	1740

QY 778 CTGACGGCGAGCTGATTAAACCAATATGTCACAAACCCAGTGAGAAGC---AAAAACCG 834
Db 781 CTGGAAGGTAAAGTTGATTAAATAATCAGTATGTGCAAAAGAGAGATGATCTTAAATAATCCA 840
QY 835 CTGACCAATTTACAAATACATCAGTTCGCGATTAAACGCGCAACCGCTTTACCGGCGAGTGCCAAAG 894
Db 841 CTGACCAATTTACAAATACATCAGTTCGCGATTAAACGCGCAACCGCTTTACCGGCGAGTGCCAAAG 900
QY 895 GTCATCTCTGATTTAGCGAAAGCGATGCGCAATAGAGAGCATTTGTTTTCATGCGCGAT 954
Db 901 GTTAGCACCGAGGTGAAGACCAACACGCTGATAAAGAAATATTTGTTTTCATACACCGAT 960
QY 955 GCCATCAGCGGCTTGAGGCGGTTTTCGCGCATAGGCGGAGAGCTTTCGCGGACGG 1014
Db 961 GCCATCAGCGGCTTGAGGCGGTTTTCGCGCATAGGCGGAGAGCTTTCGCGGACGG 1020
QY 1015 TTTATCAGCAACGCAACAGCGTATTCGGTGATTTTCGCGAGCAACCA 1061
Db 1021 TTTATCAGCAACGCAACAGCGTATTCGGTGATTTTCGCGAGCAACCA 1080
QY 1062 -----AAATAGCCCGTGCCTGCTGGAACACACCAAAATCTTGAT 1104
Db 1081 GCAAAACGATCAGATACAAATCCTGCCCTGCGCTGCGAAACACACCAAAATCTTGAT 1140
QY 1105 TCTCTGAAATTTCCGTTGATGAGCGAAGTGTGAAATCCCGACCGTTTGCCATTTCT 1164
Db 1141 TCTCTGAAATTTCCGTTGATGAGCGAAGTGTGAAATCCCGACCGTTTGCCATTTCT 1200
QY 1165 CCTATGCCCGATTTTGGTCATCCGACAAATCTTCTGCGAAGGCGATGAAATTCCTTTG 1224
Db 1201 ACTATGCCCGATTTTGGTCATCCGACAAATCTTCTGCGAAGGCGATGAAATTCCTTTG 1260
QY 1225 GTTAGCAGGAAACCATCAGCTTCGCGACGCGAGGAAATGACCGTCAGTCTTGT 1284
Db 1261 GTTAGCAGGAAACCATCAGCTTCGCGACGCGAGGAAATGACCGTCAGTCTTGT 1320
QY 1285 TGCGATTTTTCGCTGTAATCTGCGAGTAAACCGACGCGCGCCGCCCAAA 1344
Db 1321 TGCGATTTTTCGCTGTAATCTGCGAGTAAACCGACGCGCGCCGCCCAAA 1380
QY 1345 CCGAAGGCGCGAGGCGAAGAGGATTCGACATTTGATAATGCGAAGAAAGCGAAGCAAA 1404
Db 1381 CCGAAGGCGCGAGGCGAAGAGGATTCGACATTTGATAATGCGAAGAAAGCGAAGCAAA 1440
QY 1405 ATCGGCGATGAAGAGAGGCGACCGAATGATGCGCGCGAGGATGAAGGCGAGCAAGAA 1464
Db 1441 ATTTCCGAAGATGATAACGCGCGAGATGAAGTCAACCGAAGAGAGGAGCTGAAGAAACC 1500
QY 1465 GACGAAGCCACAGAAACCGAAGCGCGAAGAA----- 1497
Db 1501 GAAGAAAGAACTGATGAAGACGAGAGAGAGAACCCGGAAGAACTGAAGAACTGAAGAA 1560
QY 1498 -----GACGAAGCTGAAGAACCTGGAAGAGAAATCTGCG---GCAAGAGGCAAC 1542
Db 1561 ACTGAAGAAACTGAAGAACTGAAGAACTGAAGAAATCTGCGGACGAGAGAGGCAAC 1620
QY 1543 GCGATTTCAACGCGATCTGCTGCTGCGGAGGCTCTAAGGCGAGGATATCAACCTT 1602
Db 1621 GCGGTTTCAGGCGAGCATCTGCGGAGGCTCTAAGGCGAGGAGGAGGAGGAGGAGGAGG 1680
QY 1603 TTCTGGAAGGTATCCGACGCGCAGAAACGAATATTTTCGCAACTGGAGAGCAGCTAT 1662
Db 1681 TTCTGGAAGGTATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
QY 1663 ACCGCGACTTGGGAAGCGGTATCGCGCAACCCATTTCAATGGGCAATCATCGGAT--- 1719
Db 1741 ACCGCGACTTGGGAAGCGGTATCGCGCGCGGTATGAAGAGGCGAAGAGGAGGAGGAGG 1800
QY 1720 -----AAAGAGCGGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1749
Db 1801 ACTAGCTCCATTCAAAAGGATAGCTATGCGAATCAAGCGCGCAAAAGCAGAAATTTGACGTT 1860
QY 1750 GATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGAGAAACCGGTGATGAACTCTGCT 1809

Db 1861 GATTTTGGTGGAGAGTCCGCTTTCAGTTAAGTTGACAGAAAAAATGATACACACCCGCT 1920
QY 1810 TTCCGTTATTGAAAACCGCGGTGATTGAGGCGAAGCGTTTCCATGCGACAGCGCGACTCGG 1869
Db 1921 TTTTATATTTGAAAAGGTTGATTGATGGCAACGTTTCCACGCTTTGGCGCGTACTCGT 1980
QY 1870 GATCAGCGCATCGACCTTTTCGCGGCGAGGTTTCGACCAACCGCAGATCTTCAAAGCTAAT 1929
Db 1981 GAAAATGGTGTGATTTGTTCTGGGCAAGTTTCGACTAATCCCAAAGTTTAAAGCCAGT 2040
QY 1930 GATCTTCGTGAGAGGAGGATTTTACGCCCGCAAGCGGAGGAAATTTGGCGGATTTAT 1989
Db 2041 AATCTTCTCGTAGAAGGAGGATTTTATGTTCCGACGCGGAGGATTTGGTGGTAAATTT 2100
QY 1990 TTCAATATGATGGAAA 2007
Db 2101 ATCGACAGTGGACCGAAA 2118

RESULT 8
AAAX23323 standard; cDNA; 2124 BP.
XX AAAX23323;
XX AC AAAX23323;
XX DT 11-JUN-1999 (first entry)
XX DE N. meningitidis strain 881607 LbpB cDNA.
XX KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
XX OS Neisseria meningitidis.
XX FH Key Location/Qualifiers
XX CDS 1. 2124
XX FT /*tag= a
XX FT /product= "LbpB"
XX FN WO9909176-A1.
XX PD 25-FEB-1999.
XX PR 10-AUG-1998; 98WO-EP005117.
XX PR 15-AUG-1997; 97GB-00017423.
XX PR 05-FEB-1998; 98GB-00002544.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX Pettersson-Fernholm AM, Tommassen JPM;
XX WPI; 1999-190165/16.
XX P-PSDB; AAW93496.
XX New lactoferrin-binding protein B polynucleotides - obtained from
XX Neisseria meningitidis, used to develop products for the diagnosis,
XX prevention and treatment of neisserial disease, e.g. meningitis.
XX Claim 2; Page 105-109; 116pp; English.
XX This invention describes novel lactoferrin-binding protein B (LbpB)
XX strains of Neisseria meningitidis. The products of this invention can be
XX used for vaccinating humans against neisserial disease e.g. meningitis.
XX Antibodies raised against the proteins of the invention can be used for
XX diagnosing or treating neisserial disease in humans. The LbpB
XX polypeptides can also be used for identifying compounds which inhibit the
XX polypeptides
XX Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

[Handwritten signature]

Query Match 59.6%; Score 1296.2; DB 2; Length 2124;
Best Local Similarity 79.0%; Pred. No. 2.5e-308;
Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;

```
QY 1 ATGTGTAACCGCAATATATGCGCGCATTTGCTTGTGCGCCCTACTTTTGGCATCTTGATC 60
DB 1 ATGTGTAACCGCAATATATGCGCGCATTTGCTTGTGCGCCCTACTTTTGGCATCTTGATC 60

QY 61 GCGCGCAATTTTCGGCGTGCAGCCCTGTGTGCAATCAACGCGCGCGGTACCCCGTCACT 120
DB 61 GCGCGCAATTTTCGGCGTGCAGCCCTGTGTGCAATCAACGCGCGCGGTACCCCGTCACT 120

QY 121 TTCAAGTCTAAGACGTTTCCCATCTCGCCGCCCTGCGCAACCTTCTTATAGAAATCAAGCCG 180
DB 121 TTCAAGTCTAAGACGTTTCCCATCTCGCCGCCCTGCGCAACCTTCTTCCGCTAGAAACAGCCG 180

QY 181 GTCAACCGGCGCGCGTTCGCTGCGGCAATGCGCTGCGCAAGCGGGAATCTGCTTTTCAT 240
DB 181 GTCAACCGGCGCGCGTTCGCTGCGGCAATGCGCTGCGCAAGCGGGAATCTGCAACTTCT 240

QY 241 CGTGAAGATGGCACGGAAATTCGAATAGCAAAACAAGCAGAGAAAGCTGTGCTTTCAA 300
DB 241 GATAAGGATGGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAGCTGTGCTTTAAA 300

QY 301 GAAGGTGATCTTCTGTTTTATACGGTTCAAAGGAATTAACCTTCAAACCTTAAAGC 360
DB 301 GAGGAAGATATCTGTTTTATACGGTTCCAAAAGAGATCAACGTGAGCAGCTTAAAGAT 360

QY 361 GAAATTCATAAAGCTGATTCGGATGTAGAAATAGGACATCAGAAAGGAATAAAAA 420
DB 361 AAAATTCGTCAACCAATCTTACGGCAGCATTTACCACATTCGGAAGAAATAAAAA 420

QY 421 TATGATATAAATTTGTAGATCAGGTTATGTATA---TGTAAAGGAAAGATGAAAT 477
DB 421 TATGATATAAATTTGTAGATCAGGTTATGTATAATAAGACGAAAGATGAAAT 480

QY 478 AAGTGAATCTGATTTACAGAGATTTTCCACCGCTTAGGTATACGGTTTGTATAT 537
DB 481 GAGTGGACTTCAAAATACAGAGATCTACCAACCGGTTTGGTTATACGGTTTGTATAT 540

QY 538 TATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGGCAACGCTGGAATATCTGCT 597
DB 541 TATTCGGAGAACATCTTCCGCAATCTTTACCGAGCGCGGACAGCTGAAATATCTCGGC 600

QY 598 AACTGGCAATATATGACGATGCAAAACGTCATCGAGCAGGTAAAGC---GGTTGCAAT 654
DB 601 AACTGGCAATATATGACCGATGCCATACGTCATCGAAACAGGAAAGCAGAGATCCTAGC 660

QY 655 GACAATTTGGGTTATACATTTATGTTAGTAAAGATGTTGTTGCAACTTCTTATGCGCT 714
DB 661 GAAGATTTGGGTTATATGCTTTATACGGTCAAAATGTCCGAGCAACTTCTTATGCTGCG 720

QY 715 AAGGATGTGCGAAGGAAAGAAACATCTGCTAAATATACGGTAGATTTTCGGTAAACAA 774
DB 721 ACTGCGGACGACCGGAGGAGGAAACATCTGCGCAATATACGGTTAAATTTCCACCAAAA 780

QY 775 ACCGTGACGGCGAGTGATTAATAACCAATATGTCAAAACCGATGAGAAGC---AAAAA 831
DB 781 ACTCTGAATGGCAAGCTGATTAATAACCAATATGTGCAAAAGAGAGATCATCTTAATAA 840

QY 832 CGCGTGACCATTTTACAATCACTCGCGATTTTAAACGGCAACCGCTTTACCGGAGTGCC 891
DB 841 CCATGACCATTTTACGATTAATCTGCAAAATTTGGACGGCAACCGCTTTACCGGAGTGCC 900

QY 892 AAGGTCAATCTGATTTAGCAAAAGCCATGCGCAATAGGAGCATTTGTTTTTCATGCC 951
DB 901 AAGGTAAACACAGAGGTGAGACGATCACGCTGATTAAGAATAATTTGTTTTTCATACC 960

QY 952 GATGCCGATCAGGGCTTGAGGGCGGTTTTTTCGCGATTAAGGGGAAGAGCTTCCGGA 1011
DB 961 GATGCCGATCAGGGCTTGAGGGCGGTTTTTTCGCGGATTAAGGGGAAGAGCTTCCGGA 1020

QY 1012 CGGTTTTATCAGCAACGACACAGCGTATTCGGTGTATTCGAGGCAACAAAA----- 1061
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DB 1021 CGGTTTTATCAGCAACGACACAGCGTATTCGGGTGTTCGAGCAACAAAAACAGAG 1080
QY 1062 -----AAATAGCCCGTCCGCTCTGAAAAACACACAAAAATCTTG 1101
DB 1081 ACAGCAAAACGATCAGATACAAATCTGCGCCCTGCGCTGAGAAACACACAAAAATCTTG 1140
QY 1102 GATTTCTCTGAAAAATTTCCGTTGATGAGGCAAGTGTGAAATCCCGACCGTTTGCCATT 1161
DB 1141 GATTTCTCTAAAAATTTCCGTTGACGAGGCAAGTGTGAAATCCCGACCGTTTGAGTT 1200
QY 1162 TCTCTATGCTCCGATTTTGGTCAATCCCGACAAACTTCTTGTGAAAGGCAATGAAATTCCT 1221
DB 1201 TCCACTATGCGCGATTTTGGTCAATCCCGACAAACTTCTTGTGAAAGGCGTGAATTCCT 1260
QY 1222 TTGTTTAGCCCAAGAGAAACCACTGAGCTTTCGCGGCGGAGAAATGACCGTCAGTCT 1281
DB 1261 TTGTTTAAACAAGAAACAAACCATCGATCTTCCGCGAGCGGAGAAATGACCGTCCGTCT 1320
QY 1282 TGTTCGACTTTTTCGACTATGTGAAACTCGGACGATAAAAACCGAACGCCCGCGGCC 1341
DB 1321 TGTTCGACTTTTTCGACTATGTGAAACTCGGACGATAAAAACCGAACGCCCGCGCTC 1380
QY 1342 AAACCGAAGCGCA-----GACCAAGAGGATTCGACATTTGATATGCGCA 1389
DB 1381 CAACCGAAGCGCAGGATGAAGAGGGGACGAAGAGGGTGTAGGCGTTGATAACGGTAA 1440
QY 1390 GAAAGCGAAGAGCAATCGCGATGAAGAGGACCAAGAGATCAGCCGCGAGAT 1449
DB 1441 GAAAGCGAAGAGCAATCGCGATGAAGAGGACCAAGAGATCAGCCGAGATGAA 1500
QY 1450 GAAGGCGAAGAGAGACGAAGCCACAGAAACGAAGACGGCGAAGACGAGCTGAA 1509
DB 1501 GACGAAGATGAAGACGAAGAGAAATTCGAAGAGAACCTGAAGAGAGCTGAAGAGAA 1560
QY 1510 GAACCTGAAGAGATTCGTCGGC---AGAAGGCAAGCGAGTTTCAAACGCTTCCTGCT 1566
DB 1561 GAACCGCAAGAGATTCGCGCAGAGAGGCAACGGCGGTTTCAGGACGATCTCTGCC 1620
QY 1567 GTCCGGAAGCCTCTAAAGCGAGGATATCGACCTTTTCTGAAAGGATTCGCGAGCA 1626
DB 1621 ACTCGGAAGCCTCTAAAGCGAGGACATCGACCTTTTCTGAAAGGATTCGCGAGCG 1680
QY 1627 GAAACGAATATTTCCGCAAACTCGAGAGCAGCTATACCGGACATTCGGAAGCGCTATC 1686
DB 1681 GAAGCGCATTTCCAAAAAAGGACGCGCATTTATCCGCGACCTTGGGAGCGCTATC 1740
QY 1687 GGC-----AAACCCATTCATCGGCAATCATCGCGATTAAGAGCGGA 1731
DB 1741 GCGGTATCGGATAGTGTACGTCCATTCAAAAAGGATAGCTATGCG---AATCAAGGGCA 1797
QY 1732 AAAGCAGTATTTTACCGTTGATTTTCGCAAGAAATCGATTTCCGGAACGCTGACGGAGAA 1791
DB 1798 AAAGCAGATTTTACCGTTGATTTTCGAGCAAGACGCTGTCGGAATGCTGACAGAA 1857
QY 1792 AACGGTGAAGACCTGCTTTCGTTATGAAAAAGCGCTGATTCGAGGCAACGCTTTCAT 1851
DB 1858 AATGATACAAACCCCGCTTTTATATGAAAAAGGTGTGATTGACGGTAAACGCTTTCAC 1917
QY 1852 GCGACAGCGCGACTCGGATGACCGCATCGACCTTTTCGCGCAGGGTTTCGACCAACCG 1911
DB 1918 GCTTTGGCGCATCTCGGAGAACGGTATTCACCTTTCTGCGGCGAGGTTTCGACTAACCCG 1977
QY 1912 CAGATCTTCAAGCTTAATGATCTTCGTGTAGAGGAGGATTTTTCGCGCGAAGCGGAG 1971
DB 1978 AAGAACTTCAAGCGCAGCAATCTTCTGTAAACAGCGGCTTTTATGCGCGCAGCGGCA 2037
QY 1972 GAATTTGGCGGTATTTATTTCAATTAATGATGGGAAATCTCTTGTGATTAATGAAGTACT 2031
DB 2038 GAATTTGGCGGTATTTATTTATTCACAGCGACCGGAAATTCGGTTCGGTATTTTGGGCGGAAA 2097
QY 2032 GAAATAAGTTGAAGC 2048
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Db	2098	AAAGATGACAGGAGGC	2114	
		RESULT 9		
		AAA81482/c		
ID	AAA81482	standard; DNA; 14652 BP.		
XX	AC			
XX	AA			
XX	04-DEC-2000	(first entry)		
DE				
DE	N. meningitidis	partial DNA sequence gnm_30 SEQ ID NO:30.		
XX				
KW	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;			
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;			
KW	Meningococcus B; MenB; ds.			
XX				
OS	Neisseria meningitidis.			
XX				
PN	WO200022430-A2.			
XX				
PD	20-APR-2000.			
XX				
PF	08-OCT-1999; 99WO-US023573.			
XX				
PR	09-OCT-1998; 98US-0103794P.			
PR	30-APR-1999; 99US-0132068P.			
XX				
XX	(CHIR) CHIRON CORP.			
PA				
XX				
PI	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;			
PI	Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;			
PI	Rappuoli R, Pizza M;			
XX				
XX	WPI; 2000-318079/27.			
DR				
XX				
PT	Isolated nucleotide sequences of Neisseria meningitidis which can be used			
PT	in the diagnosis and treatment of N. meningitidis infection and other			
PT	Neisserial infections, for example, N.gonorrhoea.			
XX				
PS	Claim 7; Page 582-586; 1760pp; English.			
XX				
CC	The present invention describes methods of obtaining immunogenic proteins			
CC	from Neisseria genomic sequences. AAA81453 to AAA82414 represent			
CC	specifically claimed Neisseria meningitidis genomic DNA sequences;			
CC	AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA			
CC	sequences and their corresponding proteins; AAA81254 to AAA81259 and			
CC	AAA81304 to AAA81321 represent PCR primers used in the isolation of			
CC	Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent			
CC	Neisseria meningitidis MenB polynucleotide ORF sequences, which are all			
CC	used in the exemplification of the present invention. The nucleic acid			
CC	sequences, protein sequences, and antibodies against them, can be used in			
CC	the manufacture of a composition. The composition can be used as a			
CC	medicament (or in the manufacture of a medicament) for treating,			
CC	preventing or diagnosing infection due to Neisserial bacteria. For			
CC	example, some of the identified proteins could be components of vaccines			
CC	against Meningococcus B; against all serotypes; and/or against all			
CC	pathogenic Neisseriae. Identification of sequences from the bacterium			
CC	will also facilitate production of biological probes, particularly			
CC	organism-specific probes. Attempts to make efficacious Meningococcus B			
CC	vaccines have failed mainly due to antigen tolerance. Multivalent			
CC	antigens have also been tried but none have successfully overcome			
CC	antigenic variability. The provision of further, complete sequences may			
CC	provide an opportunity to identify secreted or surface exposed proteins			
CC	that may be presumed targets for the immune system and which are not			
CC	antigenically variable or at least more conserved than other more			
XX	variable regions			
XX				
XX	Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;			
XX				
XX	Query Match			
XX	Best Local Similarity 46.5%; Score 1010.4; DB 3; Length 14652;			
XX	Matches 1273; Conservative 82.9%; Pred. No. 1.2e-237;			
XX	0; Mismatches 176; Indels 87; Gaps 7;			

QY 1720 AAAAGACGGCGAAACAGCATATTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAACG 1779
|||
Db 13587 AAAAGACGGCGAAACAGCATATTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAACG 13528
|||
QY 1780 CTGACCGGAGAAACCGGTAGAACCTGTTCCGTTATTCGAAACCGCGGTGATTGAGGCG 1839
|||
Db 13527 CTGACCGGAGAAACCGGTAGAACCTGTTCCATATTTGAAACCGCAAGATTGAGGCG 13468
|||
QY 1840 AACGGTTTCATCCGACAGCGGCACCTCCGGATGACGGCATCGACCTTCCGGGCGAGGGT 1899
|||
Db 13467 AACGGTTTCATCCGACAGCACGACCTCCGGAGACGGCATCAATCTTCGGGAATGGT 13408
|||
QY 1900 TCGACCAACCGCAGATCTTCAAAGTAATGATCTTCGTGTAGAGAGGATTTACGGC 1959
|||
Db 13407 TCGACCGACCCCAAAACCTTCCAAGCTAGTAATCTTCGTGTAGAGGGAATTTACGGC 13348
|||
QY 1960 CCGAAGCGGAGAAATGGCGGTATATTTTCAATAATGATGGGAATCTCTTGATATA 2019
|||
Db 13347 CCGCAGCGGAGAAATGGCGGTATATTTTCAATAATGATGGGAATCTCTTGATATA 13288
|||
QY 2020 ACTGAAGGTACTGAAAATAAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTT 2079
|||
Db 13287 ACTGAAGGTACTGAAAATAAAGTTGATGTTGAAGCTGAAGTTGATGCTGAAGTTGATG 13229
|||
QY 2080 GATGCTGATGCTGATGTTGAACAGTTAAACCTGAAGTTAAACCCCAATTCGGCGTGGTA 2139
|||
Db 13228 -----TGGCAACACAGTTAGAAATCTGAAGTTAAACACCAATTCGGCGTGGTA 13183
|||
QY 2140 TTCGGTCCGAGAAACATATAAGAGGTGGAATA 2175
|||
Db 13182 TTCGGTCCGAGAAACATATAAGAGGTGGAATA 13147
|||

RESULT 10

AAF91389
ID AAF91389 standard; DNA; 1000 BP.
XX AAF91389;
AC AC
XX AC
DT 04-MAY-2001 (first entry)
XX 04-MAY-2001 (first entry)
DE N. meningitidis (serogroup B) lbpA gene upstream sequence, SEQ ID:15.
XX
XX Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine; genetically modified; protective antigen expression; LPS detoxification; LPS; lipid A; homologous recombination vector; immunisation; immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
XX
XX Neisseria meningitidis.
XX
XX WO200109350-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-EP007424.
XX
XX 03-AUG-1999; 99GB-00018319.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Berthet FJ, Dalemans WLJ, Dencel P, Dequesne G, Feron C, Lobet Y; Poolman J, Thiry G, Thonnard J, Voet P;
XX
XX WPI; 2001-138654/14.
XX
XX New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination of microbial infections.
XX
XX Claim 46; Page 81; 128pp; English.
XX
XX The invention relates to a genetically-engineered outer membrane vesicle (bleb) preparation from a Gram-negative bacterium for use as a vaccine.
CC

CC The blebs of the invention are improved with respect to their immunogenicity and toxicity by the introduction of one or more genetic changes to the chromosome of the bacterium from which the blebs are derived. The changes made include the upregulation of protective antigen expression, the downregulation of immunodominant non-protective antigen expression, and genetic changes which result in detoxification of the Lipid A moiety of lipopolysaccharide (LPS). The invention also encompasses modified Gram-negative bacterial strains from which the bleb preparations are made, a vector suitable for performing recombination events (for the generation of the modified bacterial strains), bacterially-derived nucleic acid sequences used in such a vector, and an immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a medicament for immunising a human host against a disease caused by infection of one or more of the following: *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Haemophilus influenzae*, *Moraxella catarrhalis*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, and *Chlamydia pneumoniae*. The invention may also be used to provide immunisation against the influenza virus. Bacterially derived nucleotide sequences of the invention are used in the performance of homologous recombination events up to 1000 bp upstream of a bacterial chromosomal gene in order to either increase or decrease expression of that gene. Immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more immunogenic, less toxic and safer, and are particularly useful for paediatric use. The present sequence represents a specifically claimed *Neisseria meningitidis* nucleic acid sequence
XX
SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
Query Match 31.2%; Score 678.6; DB 4; Length 1000;
Best Local Similarity 82.4%; Pred. No. 1.6e-156;
Matches 830; Conservative 0; Mismatches 164; Indels 13; Gaps 4;
QY 1174 GATTTTGGTTCATCCCGACAAACTTCTTGTGCAAGGCGATGAAATTCCTTTGGTTAGCCAA 1233
|||
Db 1 GATTTTGGTTCATCCCGACAAAGCTTCTTGTGCAAGGCGGTGAAATTCCTTTGGTTAGCCAA 60
|||
QY 1234 GAGAAAACCATCGAGCTTCCCGACGGCAGAAAATACCGTTCAGTCTTGTTCGCACTTT 1293
|||
Db 61 GAGAAAACCATCAAGCTTCCGATGCGAGGAAATGACCGTCCGTCTTTCGCACTTT 120
|||
QY 1294 TTGACCTATGTGAACTCGGACGGATATAAACCGAACGCCGCCGCCAACCGAAGGCG 1353
|||
Db 121 TTGACCTATGTGAACTCGGACGGATATAAACCGAACGCCGCCGCCAACCGAAGGCG 180
|||
QY 1354 CAGGACGAA---GAGGATTCCGACATTTGATTAATGGCGAAGAAAGCAAGCAAAATCGGC 1410
|||
Db 181 GAGATAAAGGAGGAGATGAGAGAGTGCAGGCGTTGTTAACTCGAAGAGCGGAGGC 240
|||
QY 1411 GATGAAGAAGAGGCGCACCGAAGATGCGCGCAGGAGATGAAGCGCAGGAAGACGAA 1470
|||
Db 241 GAAATTTCCGAAAGATGAAGCGGAAAGAGCGCGAAGAAATCGTCGAGAAAGAACCCGAGAA 300
|||
QY 1471 GCCACAGAAACGAGACGGCGAGAGACGAGCTGAGAGACCTGAGAGAGATCGTCG 1530
|||
Db 301 GAAGCTGAAGAGAGAAAGCTGAACCCCAAGAGATTGAAGAAACCCGAGAAATTCGCCG 360
|||
QY 1531 GCAGAAAGCAACGGCA---GTTCAAAACGGCATCTCTGCTGTCCCGAAGCCTCTAAAGGC 1587
|||
Db 361 ACAGAGAAAGCGGACGCGGTTCAACAGCCATCTCTGCTCGCTCGAAGCCTCTAAAGGC 420
|||
QY 1588 AGGGATATCGACCTTTTCTGAAAGGTATCCGCAACGGCAGAAACGAAATTCGCGAAACT 1647
|||
Db 421 AGGGACATCGACCTTTTCTGAAAGGTATCCGCAACGGCAGCGGAGCCGACATTCGAAAGAAC 480
|||
QY 1648 GGAAGAGCGCTATACCGGCATCTCGGAAGCCGCTATCGGCAACCCATTCATATGGGAC 1707
|||
Db 481 GGAAGAGCGCTATACCGGCATCTCGGAAGCCGCTATCGGCAACCCATTCATATGGGAC 540
|||
QY 1708 AATCATCGCGGATAAAGAGCGGCAAAAGCAGTATTTACCGTTGATTTCCGCAAGAAATCG 1767
|||
Db 541 AATCATCGCGGATAAAGAGCGGCAAAAGCAGTATTTACCGTTGATTTTCGCGGAGAAATCG 600
|||

QY 1768 ATTTCCGGAACCTGACGAGAGAAAAACGGTGTAGAACCTGCTTTCGGTATTGAAACGGC 1827
 DB |||||
 QY 601 ATTTCCGGAACCTGACGAGAGAAAAACGGTGTAGAACCTGCTTTCGGTATTGAAACGGC 660
 DB |||||
 QY 1828 GTGATTGAGGGCAACGGTTTCCATCGACGAGCGGCACTCGGGATGACGGCATCGACCTT 1887
 DB |||||
 QY 661 AAGATTGAGGGCAACGGTTTCCATCGACGAGCGGCACTCGGGATGACGGCATCAATCTT 720
 DB |||||
 QY 1888 TCGGGCAGGGTTCACCAACCGCAGATCTTCAAGCTAATGATCTTGGTGTAGAGGA 1947
 DB |||||
 QY 721 TCGGGAATGGTTGACCAACCCGAGACCTTCCAAAGCTAGTGTCTTGGTGTAGAGGA 780
 DB |||||
 QY 1948 GGATTTTACGGCCCGAAGCGGAGGAATGGGCGGTATTATTTCATAAATCATCGGAAA 2007
 DB |||||
 QY 781 GGATTTTACGGCCCGCA-GCGAGGAATGGGCGGTATTATTTCATAAATCATCGGAAA 839
 DB |||||
 QY 2008 TCTCTTGTATTAACCTGAAGTACTGAAATATAAAGTTGAAGCTGATGTTGATGTTGATGTT 2067
 DB |||||
 QY 840 TCTCTTGTATTAACCTGAAGTACTGAAATATAAAGTTGAAGTGAAGCTGAAGTTGAAGTT 899
 DB |||||
 QY 2068 GATGTTGATGTTGATGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 2127
 DB |||||
 QY 900 GAAGCTGAACCTGGTGTGTCGAACAGTTAGAAC-----CTGATGAAGTTAAACCCCAA 953
 DB |||||
 QY 2128 TTCCGCGTGGTATTTCGGTGCAGAGAAAGATAATAAAGAGGTGGAATA 2174
 DB |||||
 QY 954 TTCGCGTGGTATTTCGGTGCAGAGAAAGATAATAAAGAGGTGGAATA 1000
 DB |||||

RESULT 11
 ABK37769
 ID ABK37769 standard; DNA; 1000 BP.
 XX
 AC ABK37769;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE DNA sequence upstream of LbpA #1 gene.
 XX
 KW Upstream sequence; ds; Antibacterial; vaccine; bleb;
 KW Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;
 KW meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;
 KW sinusitis.
 XX
 OS Neisseria meningitidis serogroup B.
 XX
 FN WO200209746-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-EP008857.
 XX
 XX 31-JUL-2000; 2000WO-EP007424.
 PR 08-FEB-2001; 2001GB-00003170.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;
 PI Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;
 XX
 DR WPI; 2002-188688/24.
 XX
 XX New immunogenic composition comprising an antigen derived from a pathogen
 PT and a blep preparation from Neisseria meningitidis, useful as a vaccine
 PT for treating or preventing disease caused by the pathogen.
 XX
 PS Disclosure; Page 84; 125pp; English.
 XX
 CC The invention relates to an immunogenic composition comprising an antigen
 CC derived from a pathogen capable of protecting a host against the
 CC pathogen, mixed with an adjuvant comprising a blep preparation derived
 CC from a Gram-negative bacterial strain. The immunogenic composition
 CC consists of N. meningitidis B blebs or N. meningitidis C polysaccharide

CC antigen. The blebs (derived from the outer membrane) may also have their
 CC toxic lipopolysaccharide (LPS) content reduced using heterologous down
 CC regulating sequences for LPS pathway genes or by up regulating genes
 CC involved in LPS synthesis suppression, by a promoter replacement
 CC technique. The immunogenic preparation is useful in the manufacture of a
 CC medicament for the treatment of a disease caused by the pathogen from
 CC which the antigen is derived (e.g. from Neisseria, meningitis and
 CC bacteraemia, from Moraxella, otitis media and pneumonia, and from H.
 CC influenzae chronic bronchitis, sinusitis, pneumonia and otitis media).
 CC The bleb derived from M. catarrhalis or from a non-typeable H. influenzae
 CC is useful as an adjuvant in an immunogenic composition comprising one or
 CC more pneumococcal capsular polysaccharides or protein antigens. The
 CC present sequence is an upstream sequence from an N. meningitidis,
 CC H. influenzae or M. catarrhalis gene involved in LPS biosynthesis, which
 CC either up regulates or down regulates sequences to which it is attached
 XX
 SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
 Query Match 31.2%; Score 678.6; DB 6; Length 1000;
 Best Local Similarity 82.4%; Pred. No. 1.6e-156;
 Matches 830; Conservative 0; Mismatches 164; Indels 13; Gaps 4;
 QY 1174 GATTTTGTGTCATCCCGACAAACTTCTGTGGAAGGCGATGAAATTCCTTTGTTAGCCAA 1233
 DB |||||
 QY 1234 GAGAAACCATCGAGCTTGGCGACGCGAGGAAATGACCGTCAGTCTTGTTCGACTTT 1293
 DB |||||
 QY 61 GAGAAACCATCAAGCTTGGCGATGGCAGGAAATGACCGTCCGTGCTTGTTCGACTTT 120
 DB |||||
 QY 1294 TTGACCTATGTCAACTCGGAGGATGAAACCGAACCGCCCGCCCAACCGAAGGCG 1353
 DB |||||
 QY 121 TTGACCTATGTCAACTCGGAGGATGAAACCGAACCGCCCGCAAGTAAACCAAGGCG 180
 DB |||||
 QY 1354 CAGGACGAA--GAGGATTCGACATTTGATATGCGAAGAAAGGAGAACGAAATCGCG 1410
 DB |||||
 QY 181 GAAGATAAAGGAGGATGAGAGAGTGCAGCGTGTGTAAGTCTGAAGAGCGCGAAGCG 240
 DB |||||
 QY 1411 GATGAAGAAGAGGACCGAGATGTCAGCGCAGGAGATGAAGCAGGCGAAGAACGAA 1470
 DB |||||
 QY 241 GAAGTTCGGAAGATGAAGGCGAAGAACCGAAGAAATCGTGAAGAAAGAACCCGAAAGAA 300
 DB |||||
 QY 1471 GCCACAGAAACGAGAGCGGCGAAGAACGAGCTGAAGACCTGAAGAACGAAATCGTCG 1530
 DB |||||
 QY 301 GAAGCTGAAGAGGAGAGAGCTGAACCCAAAGAGTTGAAGAACCCGAGAAATTCGCGC 360
 DB |||||
 QY 1531 GCAGAGGCAACGGCA---GTTCAAACGCCATCTTCCTGCTGTCGCGAAGCCCTCTAAAGCG 1587
 DB |||||
 QY 361 ACAGAAAGAAAGCGCAGCGGTTCAAACGCCATCTTCCTGCTGCGAAGCCCTCTAAAGCG 420
 DB |||||
 QY 1588 AGGGATATCGACCTTTTCTGAAAGGTATCCGACGCGAAGAACGAAATATTCGCAAACT 1647
 DB |||||
 QY 421 AGGGATATCGACCTTTTCTGAAAGGTATCCGACGCGGAGAACGAGACATTCGAAGAAC 480
 DB |||||
 QY 1648 GGAGAACGACGCTATACCGGCATTTGGGAAGCGCTGTCGGCAACCCCATTCATGGGAC 1707
 DB |||||
 QY 481 GGAAAGCACATATACCGGCATTTGGGAAGCGGTATCGGCACACCCCATTCATGGGAC 540
 DB |||||
 QY 1708 AATCATGCGGATTAAGAGAGCGGCAAAAGCAGTATTACCGTTGATTCGCGAAGAAATCG 1767
 DB |||||
 QY 541 AATCAGCGCGATTAAGAGCGGCAAAAGCAGTATTACCGTTGATTCGCGGAGAAATCG 600
 DB |||||
 QY 1768 ATTTCCGGAACGCTGACGAGGAAACCGGTGTAGAACCTGCTTTCGGTATTGAAACCGCG 1827
 DB |||||
 QY 601 ATTTCCGGAACGCTGACGAGGAAACCGGTGTAGAACCTGCTTTCGGTATTGAAACCGCG 660
 DB |||||
 QY 1828 GTGATTGAGGGCAACGGTTTCCATGCGACGCGCACTCGGATGAGGATCGACCTT 1887
 DB |||||
 QY 661 AAGATTGAGGGCAACGGTTTCCATGCGACGCGCACTCGGATGAGGATCGATCAATCTT 720
 DB |||||
 QY 1888 TCCGGGCGAGGTTCCGACCAACCGCAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGA 1947
 DB |||||
 QY 721 TCGGGAATGGTTGACCAACCCGAGACCTTCCAGCTAGTATCTTCGTGTAGAGGA 780
 DB |||||

QY 1948 GGATTTTACGGCCCGGAGGCGGAGGAATTTGGCGGTATTTTTCATATGATGGAAA 2007
Dd |||||
781 GGATTTTACGGCCCGCA-GCGAGAGGATTTGGCGGTATTTTTCATATGATGGAAA 839
QY 2008 TCTCTTGGTATAACTGAAGTACTGAAATPAAGTTGAAGCTGATGTTGATGTT 2067
Dd |||||
840 TCTCTTGGTATAACTGAAGTACTGAAATPAAGTTGAAGTTGAAGTTGAAGTT 899
QY 2068 GATGTTGATGTTGATGCTGATGCTGATGTTGAACAGTTAAACCTGAAGTTAAACCCAA 2127
Dd |||||
900 GAAGCTGAACACTGGTGTGTCGAACAGTTAGAAC-----CTGATGAAGTTAAACCCCAA 953
QY 2128 TTCCGGCGTGTATTCGGTGCAGAAAGATAATAAGAGGTGGAATA 2174
Dd |||||
954 TTCCGGCGTGTATTCGGTGCAGAAAGATAATAAGAGGTGGAATA 1000

RESULT 12
AAA81815
ID AAA81815 standard; DNA; 707 BP.
XX
AC AAA81815;
XX
DT 04-DRC-2000 (first entry)
XX
DE N. meningitidis partial DNA sequence gpm_362 SEQ ID NO:362.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
OS Neisseria meningitidis.
XX
PN WC200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US023573.
XX
PR 09-OCT-1998; 98US-0103794P.
PR 30-APR-1999; 99US-0132068P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisserial infections, for example, N.gonorrhoea.
XX
PS Claim 7; Page 1606; 1760pp; English.
XX
CC The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium

CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX
SQ Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;
Query Match 21.2%; Score 460.4; DB 3; Length 707;
Best Local Similarity 79.3%; Pred. No. 6.4e-103;
Matches 561; Conservative 0; Mismatches 137; Indels 9; Gaps 1;
QY 23 GCATTTGCTTTGTTGGCCCTTACTTTTGGCATCTTTGTATCGCGCAATTTTGGCGTGCAGC 82
Dd |||||
1 GCATTTGCTTTGTTGGCCCTTACTTTTGGCATCTTTGTATCGCGCAATTTTGGCGTGCAGC 60
QY 83 CTGTTGTGCAATCAACGCGCAGCCGCTACCCCGTCACTTTCAAGTCTTAAGGACGTTCCCA 142
Dd |||||
61 CTGTTGTGCAATCAACGCGCAGCCGCTACCCCGTCACTTTCAATCTTAAGGACGTTCCCA 120
QY 143 CTCGCCCCCTGCCAAACCTTTTATAGAAATACGCCGCTCAACCGCCCGCGTCCGGT 202
Dd |||||
121 CTCGCCCCCTGCCGGGTCTTCGGTAGAAACACCGCGGTCAACCGCCCGCGTCCGGT 180
QY 203 CGCAATGCGGTGCCAAGCGCAATCTGCTTTTCATCGTGAAGTGGCACGGAATTC 262
Dd |||||
181 CGCAATGCGGTGCCAAGCGCAATCTGCTTTTCATTAACCAAGACGCTACCGAAATTC 240
QY 263 CAAATAGCAAAACGAGCAAGAAAGCTGCTGCTTTCAAGAGGTGATGTTCTGTTTTAT 322
Dd |||||
241 CCGACAGCATCAGGACAGGAGCATCTGCCGTTTAAAGAGAGGATATCTGTTTTAG 300
QY 323 ACGGTTCAAAAGGAATAAACTTCAACAACTTAAAAAGCGAAATTCATAACGTAATTCG 382
Dd |||||
301 ACGGTTACGCTGAAAGAACAGGCTGACAACTTAAAAAGAAATCAACGAAACGGTATTCG 360
QY 383 ATGTAGAAATTAGGACATCAGAAAGGAATTAAGAAATATGATTATAATTTCTAGATG 442
Dd |||||
361 ATGTAGGGGTATCATCATCGAAAAAGAGAAAGAAATATCAATATCAATTTGTCGGTG 420
QY 443 CAGGTTATGATATGTAAGGGGAAAG-----ATGAAATTAAGTGGACTTCAGATT 493
Dd |||||
421 CGGCTATGTTTACCAGCGCGGAGGAGGATATGAAAGAAAGACATTCGATG 480
QY 494 ACAAGCAGTTTCCAAACCGCTTAGGTTATGACCGGTTTGTATATATTCGCGAGACGTC 553
Dd |||||
481 GTAAGGAGTTTGTAAACCGATTAGTTATGACGGTTTGTATATATTCGCGAGACGTC 540
QY 554 CTTCCCAATCTTTACCGAGTCCGGAACGGTGAATATTTCTGTAATCGCAATATATGA 613
Dd |||||
541 CTTCCCAATCTTTACCGAGCGCGGAAACGGTGAATATTCGCGTAATCGCAATATATGA 600
QY 614 CCGATGCCAAACGCTCATCGAGCAGTAAAGCGGTTCGCATTGCAATTTGGGTTATATCA 673
Dd |||||
601 CCGATGCCAAACGCTCATCGGACANGTAAGCGGTTTCAGTACGATTGGGTTATATCA 660
QY 674 CATTATGATGAACGATGTTGGTGCAACTTCTTATCGCGCTAAGGAT 720
Dd |||||
661 CATATTATGTAATGAAATTTGGGCAACTTCTTATGAGGCTAGGAT 707

RESULT 13
ABS67377
ID ABS67377 standard; DNA; 3300 BP.
XX
AC ABS67377;
XX
DT 29-NOV-2002 (first entry)
XX

[illegible]

Search completed: August 23, 2004, 19:47:01
Job time : 849 secs

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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 19:32:53 ; Search time 156 Seconds

(without alignments)
7737.296 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175

Sequence: 1 atgtgtaaacggaattatgg.....ataataaagggtggaaaaa 2175

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.2	4.1	2139	4	US-09-059-584-50
2	78.2	3.6	7218	1	US-08-232-463-14
3	75.4	3.5	2121	4	US-09-059-584-45
4	75.4	3.5	2127	4	US-08-778-570B-8
5	75.4	3.5	2127	4	US-09-059-584-8
6	75.4	3.5	3435	4	US-08-778-570B-7
7	75.4	3.5	3435	4	US-09-059-584-7
8	71	3.3	2230	3	US-08-448-194-7
9	71	3.3	2230	4	US-08-867-921-7
10	70.8	3.3	2145	4	US-09-059-584-48
11	70.8	3.3	2287	4	US-09-059-584-47
12	70.8	3.3	58909	4	US-09-596-002-30
13	69.2	3.2	929	4	US-09-671-317-14
14	69.2	3.2	1001	4	US-09-671-317-439
15	67.6	3.1	390	3	US-09-197-649-7
16	67.6	3.1	1276	3	US-09-177-325-2
17	67.6	3.1	1276	3	US-09-411-812A-2
18	67.6	3.1	1276	4	US-09-590-113-2
19	66.4	3.1	2256	6	5220013-1
20	65	3.0	2223	1	Sequence 4, Appl
21	65	3.0	43795	3	US-08-257-073-4
22	64.8	3.0	2253	4	US-08-742-185-101
23	64.8	3.0	2253	4	US-09-548-372D-56
24	64.8	3.0	2253	4	US-09-548-367D-56
25	64.8	3.0	2256	2	US-09-551-853D-56
26	64.8	3.0	2256	2	US-08-422-333-1
27	64.8	3.0	2256	6	5187153-1
					Patent No. 5187153
					Patent No. 5223482-1

28 64.8 3.0 2259 4 US-09-548-372D-60 Sequence 60, Appl
29 64.8 3.0 2259 4 US-09-548-367D-60 Sequence 60, Appl
30 64.8 3.0 2259 4 US-09-551-853D-60 Sequence 60, Appl
31 64.8 3.0 2265 2 US-08-104-165-5 Sequence 5, Appl
32 64.8 3.0 2265 3 US-08-464-250-5 Sequence 5, Appl
33 64.8 3.0 2265 4 US-08-464-250-5 Sequence 5, Appl
34 64.8 3.0 2310 4 US-09-548-372D-54 Sequence 54, Appl
35 64.8 3.0 2310 4 US-09-548-367D-54 Sequence 54, Appl
36 64.8 3.0 2310 4 US-09-551-853D-54 Sequence 54, Appl
37 64.8 3.0 2310 4 US-08-685-849-2 Sequence 2, Appl
38 64.8 3.0 2313 1 US-08-133-248-7 Sequence 7, Appl
39 64.8 3.0 2316 4 US-09-548-372D-58 Sequence 58, Appl
40 64.8 3.0 2316 4 US-09-548-367D-58 Sequence 58, Appl
41 64.8 3.0 2316 4 US-09-551-853D-58 Sequence 58, Appl
42 64.8 3.0 3148 1 US-08-133-702-3 Sequence 3, Appl
43 64.8 3.0 3148 4 US-08-832-867-4 Sequence 4, Appl
44 64.8 3.0 3520 2 US-08-422-333-20 Sequence 20, Appl
45 64.8 3.0 8591 1 US-08-462-859A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-059-584-50
; Sequence 50, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2139 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-059-584-50
Query Match 4.1%; Score 88.2; DB 4; Length 2139;

Best Local Similarity 57.3%; Pred. No. 5e-13;
Matches 184; Conservative 0; Mismatches 128; Indels 9; Gaps 1;
QY 747 TAAATACGGTAGATTTCGGTAACAAACCCCTGACGGCGAGCTGATTAACAAACCAATA 806
Db 978 TGTGTTACGGTAGATTTCGGTAACAAACCCCTGACGGCGAGCTGATTAACAAACCAATA 1037
QY 807 TGTCAAACCCAGTGTGAAGCAAAACCGCTGACCATTTTAAACATCACTGCCGATTTAAA 866
Db 1038 AGACCAACCAATAGGGCAAGGTACGAACAAACCAACGCTATGACATCAATGCCGATATCA 1097
QY 867 CGGCAACCGTTTACCGGAGTCCCAAGGTCAATCTGATTAGCGAAAGCAATGCCAA 926
Db 1098 CGGTAACCGTTTCCGTTGGCAGTCCCAACCGCAATCAATCAATCAATCAATCAATCAAT 1157
QY 927 TAAGGAGCATTTGTTTTCATGCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 986
Db 1158 ACA-----CCCCCTTTACCGAGTCCGATCCGATCCGATCCGATCCGATCCGATCCG 1208
QY 987 CGATAAGGGGAGAGCTTGCAGGAGCGTTTATCAGCAACGACAAACAGCGTATTCGGTGT 1046
Db 1209 ACCAAGCGCGAGGAGCTGCGAGTAAATTCCTAACCGATGACAAACAACTCTTTGGTGT 1268
QY 1047 ATTCGAGGCAACAAATAG 1067
Db 1269 CTTTGGTGCTAAACAAGAG 1289

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
; US-08-232-463-14
Query Match 3.8%; Score 78.2; DB 1; Length 7218;
Best Local Similarity 5.7%; Pred. No. 3.7e-10;
Matches 23; Conservative 237; Mismatches 145; Indels 0; Gaps 0;
QY 1174 GATTTTGGTCATCCCGACAAACTTCTGTGCGAGGCGATCAAAATTCCTTTGGTAGCCAA 1233
Db 1445 GAATTTGGTAGCTACRR 1386
QY 1234 GAGAAACCATCGAGCTTGCAGCGACGAGGAAATGACCGTCAGTGTCTTGTTCGCACTTT 1293
Db 1385 RRR 1326
QY 1294 TTGACCTGTGAATCTCGACGATGATAAAACCGAACCGCCCGCCGCAACCGAAGCG 1353
Db 1325 RRR 1266
QY 1354 CAGGACGAAGAGATTTCGGACATTTGATAATGGCGAAGAAAGCGAAGCAAAATCGCGAT 1413
Db 1265 RRR 1206
QY 1414 GAAGAAAGAGCGACCGAAGATGACCGCGAGGAGATGAAGCGAGCGAAGCAAGCG 1473
Db 1205 RRR 1146
QY 1474 ACAGAAACGAAGCGCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1533
Db 1145 RRR 1086
QY 1534 GAAGCAAGCGAGTTTCAAAACCGCATCTTCTGCTGCTCCCGAAGCC 1578
Db 1085 RRR 1041

RESULT 3
US-09-059-584-45
; Sequence 45, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Leosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I

REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-794
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-059-584-45

Query Match 3.5%; Score 75.4; DB 4; Length 2121;
Best Local Similarity 48.2%; Pred. No. 1.1e-09;
Matches 251; Conservative 0; Mismatches 261; Indels 9; Gaps 1;

QY 747 TAAATATACGTTAGATTTCGGTAAACAAACCCCTGACGGGCGAGCTGATTAAACCAATA 806
Db 1008 TGATTTACTGTTAAATTTAAGGACAAAATTAACAGGTGAGCTGTTTAGTAACCTACA 1067
QY 807 TGTCAAAACCCAGTGAGAGCAAAACCGCTGACCATTTTACAATCATCTGCCGATTAAA 866
Db 1068 AGACAGCGGTAGGGCAATGTTACGAAACCAACAGCTATGACATCGATGCCATATCTA 1127
QY 867 CGGCAACCGCTTACCGGAGTGCACAGTCAATCTGATTAGCGAAAGCCATGCCAA 926
Db 1128 CGGCAACCGCTTCGGTGGCAGTGCCACCGCAAGCGATAAAGCAGAAAGCAACCA 1187
QY 927 TAGGAGCATTTGTTTTTCCATGCCGATCGGCTGAGGCGCTTTCGGCGGTTTCGG 986
Db 1188 ACACCCC-----TTTACCAGCGATGCCAAATAGCTAGAGCGGCTTTTATGG 1238
QY 987 CGATAGGGGAGAGCTTCCGAGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGT 1046
Db 1239 ACCAAACCGCGAGGCTGCGAGGTAAATTCCTAACCAATGACAAACAACTCTTTGGCGT 1298
QY 1047 ATTCGAGGCAAAACAAATAGCCCGCTGCGTCTGGAAACACACCAAAATCTTGGATTC 1106
Db 1299 CTTTGGTGCTAAACGAGAGAGTAAAGCTGGGGAACAAACCGAACCATCTTAGATGCCA 1358
QY 1107 TCTGAAATTCCTGATGAGGCAAGTGTGAAATCCCGAGCGTTTGGCAATTTCTCC 1166
Db 1359 TGCATTTGGGACATTTAACAATAATAGCAACCACTACCCCATTTACCAAAACA 1418
QY 1167 TATCCCGATTTTGGTATCCCGACAAACTCTTTGTGAGAGGCGATGAATTCCTTTGGT 1226
Db 1419 ACTGATAAATCTTGGCAATGCCAAAGTTGGTCTTGGGTTCTACCGCTCATTTGATTTGGT 1478
QY 1227 TAGCAGAGAAACCATCGAGCTTGGCAGCGGAGNAAA 1267
Db 1479 GCCTACCGGTGTCACCAAGATGTCATGAATTCACCAAAA 1519

RESULT 4

US-08-778-570B-8
Sequence 8, Application US/08778570B
Patent No. 6437096

GENERAL INFORMATION:

APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario

COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-664
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-778-570B-8

Query Match 3.5%; Score 75.4; DB 4; Length 2127;
Best Local Similarity 54.8%; Pred. No. 1.1e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 747 TAAATATACGTTAGATTTCGGTAAACAAACCCCTGACGGGCGAGCTGATTAAACCAATA 806
Db 1011 TGATTTACGTTAGATTTTTAGTAAAGAGCTTAAAGGTGAGCTGCTAGTAACATACA 1070
QY 807 TGTCAAAACCCAGTGAGAGCAAAACCGCTGACCATTTTACAATCATCTGCCGATTAAA 866
Db 1071 AGACGGCATTAAGGGCAGTGTTAATAAACCAACCGCTATGACATCGATGCCATATCTA 1130
QY 867 CGGCAACCGCTTACCGGAGTGCACAGTCAATCTGATTAGCGAAAGCCATGCCAA 926
Db 1131 CGGCAACCGCTTCGGTGGCAGTGCCACCGAGCGATACACAGCAAGCAAGCA 1190
QY 927 TAAGAGCATTTGTTTTTCCATGCCGATCGCGATCAGCGCTTTCGGCGGCTTTTCGG 986
Db 1191 ACACCCC-----TTTACCAGCGATGCCAAATAGCTAGAGCGGCTTTTATGG 1241
QY 987 CGATAGGGGAGAGCTTGGCGAGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGT 1046
Db 1242 ACCAAACCGGAGAGCTGGCAGGTAATTCCTAACCAATGACAAACAACTCTTTGGCGT 1301
QY 1047 ATTCGAGGCAACCAAAATAG 1067
Db 1302 CTTTGGTGCTAACGAGAG 1322

RESULT 5

US-09-059-584-8
Sequence 8, Application US/09059584
Patent No. 6440701

GENERAL INFORMATION:

APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto

```

; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-8

```

Query Match 3.5%; Score 75.4; DB 4; Length 2127;

Best Local Similarity 54.8%; Pred. No. 1.1e-09;

Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

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QY 747 TAAATATAGGTAGTATTCGGTAAACAAACCTGACGGCGAGCTGATTAATAAACCAATA 806
Db 1011 TGAGTTTACGGTAGATTTTAGTAAAGAGCCGTAAAGGTGAGCTGTCTAGTAACATACA 1070
QY 807 TGTCAAAACCCAGTGAAGACAAACCCGCTGACCATTTTACACATCACTGCCGATTTAAA 866
Db 1071 AGACGGCCATAAGGCGAGTGTATTAATAACCAACGCTATGATCGATGCCAATATCTA 1130
QY 867 CGGCAACCGCTTTACCGGAGTGCCAGAGTCAATCTGATTTAGCGAAAGCCATGCCAA 926
Db 1131 CGGCAACCGCTTTCCGTTGGCAGTGCCACCGCAAGCGATACAACAGAGCAAGCAAAAGCAA 1190
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCGCCGATGAGGCGGTTTTTTCGG 986
Db 1191 ACACCCC-----TTTACCAGCGATGCCAAATAGCCCTAGAGGCGGTTTTTATGG 1241
QY 987 CGATAAGGGGAAGAGCTTGGCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGT 1046
Db 1242 ACCAAACCGCGAGAGCTGGCAGGTAAATCTCTAACCAATGACAACAACCTTTGGCGT 1301
QY 1047 ATTGCGAGGCAACAAATAG 1067
Db 1302 CTTTGGTCTAAACGAGAG 1322

```

RESULT 6

US-08-778-570B-7

; Sequence 7, Application US/08778570B

; Patent No. 6437096

; GENERAL INFORMATION:

; APPLICANT: Myers, Lisa E

; APPLICANT: Schryvers, Anthony B

; APPLICANT: Harkness, Robin E

; APPLICANT: Loosmore, Sheena M.

; APPLICANT: Du, Run-Pan

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Klein, Michel H

; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella

```

; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,570B
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-664
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-778-570B-7

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Query Match 3.5%; Score 75.4; DB 4; Length 3435;

Best Local Similarity 54.8%; Pred. No. 1.4e-09;

Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

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QY 747 TAAATATAGGTAGTATTCGGTAAACAAACCCCTGACGGCGAGCTGATTAATAAACCAATA 806
Db 1703 TGAGTTTACGGTAGATTTTAGTAAAGAGCCGTAAAGGTGAGCTGTCTAGTAACATACA 1762
QY 807 TGTCAAAACCCAGTGAAGACAAACCCGCTGACCATTTTACACATCACTGCCGATTTAAA 866
Db 1763 AGACGGCCATAAGGCGAGTGTATTAATAACCAACGCTATGATCGCAATATCTA 1822
QY 867 CGGCAACCGCTTTACCGGAGTGCCAGAGTCAATCTGATTTAGCGAAAGCCATGCCAA 926
Db 1823 CGGCAACCGCTTTCCGTTGGCAGTGCCACCGCAAGCGATACAACAGAGCAAGCAAAAGCAA 1882
QY 927 TAAGGAGCATTTGTTTTTCCATGCCGATGCCGATCGCCGCTTGAAGGCGGTTTTTTCGG 986
Db 1883 ACACCCC-----TTTACCAGCGATGCCAAATAGCCCTAGAGGCGGTTTTTATGG 1933
QY 987 CGATAAGGGGAAGAGCTTGGCGGACGGTTTATCAGCAACGACAAACAGCGTATTCGGTGT 1046
Db 1934 ACCAAACCGCGAGAGCTGGCAGGTAAATCTCTAACCAATGACAACAACCTTTGGCGT 1993
QY 1047 ATTGCGAGGCAACAAATAG 1067
Db 1994 CTTTGGTCTAAACGAGAG 2014

```

RESULT 7

US-09-059-584-7

; Sequence 7, Application US/09059584

; Patent No. 6440701

; GENERAL INFORMATION:

; APPLICANT: Myers, Lisa E

; APPLICANT: Schryvers, Anthony B

; APPLICANT: Harkness, Robin E

; APPLICANT: Loosmore, Sheena M.

; APPLICANT: Du, Run-Pan

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Klein, Michel H

; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella

; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3435 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-059-584-7

Query Match 3.5%; Score 75.4; DB 4; Length 3435;
Best Local Similarity 54.8%; Pred. No. 1.4e-09;
Matches 176; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

Qy	747	TAAATATACGCTAGATTTCGGTAAACAAACCCCTGACGGCGAGCTGATTAAAAACCAATA	806
Db	1703	TGAGTTACGCTAGATTATTAGTAAAGAGCGCTAAAGGTGAGCTGTCTAGTAACATACA	1762
Qy	807	TGTCAAACCCGCTGAGAGACGAAACCCGCTGACCATTTACAAATCAGTCCGATTTAAA	866
Db	1763	AGACGGCCATAAGGCGAGTGTAAATAAAACCAACGCTATGACATCGATGCAATATCTA	1822
Qy	867	CGGCAACCGCTTACCGCGAGTGCCAGGTCAATCTGATTTAGCGAAAGCCATGCCAA	926
Db	1823	CGGCAACCGCTTCCGTGGCGAGTGCCAGGTCAATCTGATTTAGCGAAAGCCATGCCAA	1882
Qy	927	TAAGGAGCATTTGTTTTTCCATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG	986
Db	1883	ACACCCC-----TTTACCAGGATGCCAAATATAGCCTAGAGCGGTTTTTATGG	1933
Qy	987	CGATAAGGGGAGAGCTTGCGGAGCGGTTTATCAGAACGACAAACAGCGTATTCGGTGT	1046
Db	1934	ACCAACCGCGAGGAGCTGGCAGGTAAATTCCTAACCAATGACAAACAACTCTTTGGGT	1993
Qy	1047	ATTCGAGGCAACCAATAG	1067
Db	1994	CTTTGGTGCTAAACGAGAG	2014

RESULT 8

US-08-448-194-7
; Sequence 7, Application US/08448194
; Patent No. 6028049
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; APPLICANT: LEBRAIN, Michele

; APPLICANT: MAZARIN, Veronique
; APPLICANT: BOUCHON-THEISEN, Bernadette
; APPLICANT: SCHREYVERS, Anthony B.
; APPLICANT: BLOCH, Marie-Aline
; TITLE OF INVENTION: DNA FRAGMENTS CODING FOR THE TRANSFERRIN
; TITLE OF INVENTION: RECEPTOR OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,194
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/361,469
; FILING DATE: 22-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,053

; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92 07493
; FILING DATE: 19-JUN-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm M.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016100-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: DNA which encodes Tbp2 subunit of transferrin

; ORGANISM: receptor
; STRAIN: Neisseria meningitidis IM2169
; FEATURE:
; NAME/KEY: sig_peptide

; LOCATION: 60..119
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 120..2192

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..2192
US-08-448-194-7

Query Match 3.3%; Score 71; DB 3; Length 2230;
Best Local Similarity 51.8%; Pred. No. 1.5e-08;
Matches 214; Conservative 0; Mismatches 190; Indels 9; Gaps 2;

Qy	1601	TTTTCTCGAAAGGTATCCGACGCGAGAAACGAATATTCGCAAACTCGAGAGCACCGCT	1660
Db	1690	TGTTCTCCAAAGCGGAGCGGTACCGATGAAAAGAGATTCCAAACGACCAACACGTCGTTT	1749
Qy	1661	ATACCGGCACATTGGGAAGCGCGGTATCGGCAAAACCAATTCATATGGGACAAATCATCGGATA	1720
Db	1750	ATCGGGGGTCTTGGTACGGGCATATTCGCAACGCGCAAGCTGGAGCGGCAATGCTTCTG	1809

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QY 1721 AAGAACGG-----CAAAAGCAGTATTTACCGTGTGATTTCCGCAAGAAATCGATTTCCG 1774
      |||||
Db 1810 AATAAGAGCGCGCAACAGGGCGGAATTTACTGTGAATTTTCCGATAAAAAATTTACCG 1869
      |||||
QY 1775 GAACGCTGACGGAGAAAACGGTGTAGAACCTCTTCCGTATTTGAAAACGGCGGTGATTG 1834
      |||||
Db 1870 GCAAGTTTAAACGCTGAAAACAGCAGCGCAACCTTTTACCAATGAG---GGAATGATTC 1926
      |||||
QY 1835 AGGCAACGCTTTCCATCGACAGCGCACTCGGATGACGCGATCGACCTTTCCGGGC 1894
      |||||
Db 1927 AGGCAACGCTTTGAGTACGCGCAAACTCTGAGTCAGTTTTTGATCTCGATCAAA 1986
      |||||
QY 1895 AGGTTTCGACCAACCCGAGATCTTCAAGCTAATGATCTTCTGTAGAGGAGGATTTT 1954
      |||||
Db 1987 AATAACCAACCGCAGCGCTAAGGCATATATACAGATGCCAAGTTAAAGGGCGGTTTTT 2046
      |||||
QY 1955 AGGCGCGAGGCGGAGGAATGGCGGTATTTTTCATATATGATGGAAA 2007
      |||||
Db 2047 ACGGCGCTAAAGCGAAGAGTTGGCGGATGGTTTGCCTATCCGGCGGATAAA 2099
      |||||

```

RESULT 9

US-08-867-921-7

; Sequence 7, Application US/08867921

; Patent No. 6326350

; GENERAL INFORMATION:

; APPLICANT: JACOBS, Eric

; APPLICANT: LEGRAIN, Michele

; APPLICANT: MAZARIN, Veronique

; APPLICANT: BOUCHON-THEISEN, Bernadette

; APPLICANT: SCHRYVERS, Anthony B.

; APPLICANT: BLOCH, Marie-Aline

; TITLE OF INVENTION: DNA FRAGMENTS CODING FOR THE TRANSFERRIN

; TITLE OF INVENTION: RECEPTOR OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/867,921

; FILING DATE: 03-JUN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/445,472

; FILING DATE: 22-MAY-1995

; APPLICATION NUMBER: US 08/361,469

; FILING DATE: 22-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/078,053

; FILING DATE: 18-JUN-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92 07493

; FILING DATE: 19-JUN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 016100-004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 2230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: DNA which encodes Tbp2 subunit of transferrin
; ORGANISM: Neisseria meningitidis IM2169
; STRAIN: Neisseria meningitidis IM2169
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 60..119
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 120..2192
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..2192
; US-08-867-921-7

```

Query Match 3.3%; Score 71; DB 4; Length 2230;

Best Local Similarity 51.8%; Pred. No. 1.5e-08; Mismatches 190; Indels 9; Gaps 2; Matches 214; Conservative 0;

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QY 1601 TTTTCTGAAAGTATCCGACGCGCAGAAACGAAATATTCGCAAACTGGAGAAAGCAGCT 1660
      |||||
Db 1690 TGTTCCTCCAAGCGAGCGGTACCGATGAAAAAGAGATTCCAACCGACCAAAACGTCGTTT 1749
      |||||
QY 1661 ATACCGGCACTTGGGAGCGCGTATCGGCAAAACCCATTCATGCGGCAATCATCGCGATA 1720
      |||||
Db 1750 ATCGGGGGTCTTGGTACGGGCGATATTGCCAACGGCAACAGCTGGAGCGCAATGCTTCTG 1809
      |||||
QY 1721 AAGAAGCGG-----CAAAAGCAGTATTTTACCGTTCGATTTGGCAAGAAATCGATTTCCG 1774
      |||||
Db 1810 ATAAAGAGGCGGCAACAGCGGCGGAATTTACTGTGAATTTGCCGATAAAAAATTTACCG 1869
      |||||
QY 1775 GAACGCTGACGAGAAAAACGGTGTAGAACCTTCTTCGTATTTGAAAAACGGCGTGATTG 1834
      |||||
Db 1870 GCAAGTTAAACGCTGAAAAACAGCGAGCGCAAAACCTTTTACCATTGAG---GGAATGATTC 1926
      |||||
QY 1835 AGGCGCAACGGTTTCCATCGACAGCGCGCACTCGGATCGGCACTCGACCTTCCGGGC 1894
      |||||
Db 1927 AGGCGCAACGGCTTTGAAGGTACGGCGCAAAACCTGCTGAGTAGGTTTGTATCTCGATCAAA 1986
      |||||
QY 1895 AGGTTTCGACCAAAACCGCAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGGATTTT 1954
      |||||
Db 1987 AATAACCAACCGCGCAGCGCTAAGGCATATATCACAGATGCCAAGTTAAAGGGCGGTTTTT 2046
      |||||
QY 1955 ACGGCGCGAAGCGGAGGAATTTGGCGGTATTATTTTCATATATGATGGAAA 2007
      |||||
Db 2047 ACGGCGCTAAAGCGAAGAGTTGGCGGATGGTTTGCCTATCCGGCGGATAAA 2099
      |||||

```

RESULT 10

US-09-059-584-48

; Sequence 48, Application US/09059584

; Patent No. 6440701

; GENERAL INFORMATION:

; APPLICANT: Myers, Lisa E

; APPLICANT: Schryvers, Anthony B

; APPLICANT: Harkness, Robin E

; APPLICANT: Loosmore, Sheena M.

; APPLICANT: Du, Run-Pan

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Klein, Michel H

; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: 6th Floor, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada


```

; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-48

Query Match 3.3%; Score 70.8; DB 4; Length 2145;
Best Local Similarity 54.1%; Pred. No. 1.7e-08;
Matches 172; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

Qy 747 TAAATATACGGTAGATTTCGGTACAAAACCCCTGACGGGCGAGCTGATTTAAAAACCAATA 806
Db 1017 TGAATTACTGTTAATTAAAGGAAAAAAATTAACAGGTGAGCTGTTTAGTAACTTACA 1076

Qy 807 TGTCAAAACCGAGTCAGAGCAAAAACCGCTGACCATTTTACAAATCACTGCCGATTTAAA 866
Db 1077 AGACAGCCATAAACAAGTAACCAAAAACGCTATGATATTAAGGCTGATATCCA 1136

Qy 867 CGGCAACCGCTTTACCGGAGTCCAAAGTCAATCTGATTAGCGAAAAGCCATGCGAA 926
Db 1137 CGGCAACCGCTTCGCTGGCATGCCACGCAACGGATAAGCGAAGACAGACAGCAAAAGCAA 1196

Qy 927 TAAGGAGCATTTGTTTTCATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 986
Db 1197 ACACCCC-----TTTACCGCCATGCCAAAGATAAGCTAGAAAGTGTTTATGG 1247

Qy 987 CGATAAGGGGGAAGAGCTTCCGCGACGGTTTATCAGCAACGACACACAGCGTATTCGGTGT 1046
Db 1248 ACCAAAAGGCGAGAGCTGGCAGGTAATTTCTTACCGATGATAACAACTCTTTGGTGT 1307

Qy 1047 ATTCGCGAGCAAAACAAA 1064
Db 1308 CTTTGGTGCCAAACAAGA 1325

RESULT 11
US-09-059-584-47
; Sequence 47, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-47

Query Match 3.3%; Score 70.8; DB 4; Length 2287;
Best Local Similarity 54.1%; Pred. No. 1.7e-08;
Matches 172; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

Qy 747 TAAATATACGGTAGATTTCGGTACAAAACCCCTGACGGGCGAGCTGATTTAAAAACCAATA 806
Db 1159 TGAATTACTGTTAATTAAAGGAAAAAAATTAACAGGTGAGCTGTTTAGTAACTTACA 1218

Qy 807 TGTCAAAACCGAGTCAGAGCAAAAACCGCTGACCATTTTACAAATCACTGCCGATTTAAA 866
Db 1219 AGACAGCCATAAACAAGTAACCAAAAACGCTATGATATTAAGGCTGATATCCA 1278

Qy 867 CGGCAACCGCTTTACCGGAGTCCAAAGTCAATCTCTGATTTAGCGAAAAGCCATGCGAA 926
Db 1279 CGGCAACCGCTTCGCTGGCATGCCACGCAACGATAAGCGAAGACAGCAAAAGCAA 1338

Qy 927 TAAGGAGCATTTGTTTTCATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 986
Db 1339 ACACCCC-----TTTACCGCCATGCCAAAGATAAGCTAGAAAGTGTTTATGG 1389

Qy 987 CGATAAGGGGGAAGAGCTTCCGCGACGGTTTATCAGCAACGACACACAGCGTATTCGGTGT 1046
Db 1390 ACCAAAAGGCGAGAGCTGGCAGGTAATTTCTTACCGATGATAACAACTCTTTGGTGT 1449

Qy 1047 ATTCGCGAGCAAAACAAA 1064
Db 1450 CTTTGGTGCCAAACAAGA 1467

RESULT 12
US-09-596-002-30
; Sequence 30, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Legace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: FM-0008-4 US

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RESULT 13
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:

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RESULT 14
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIOMIMETIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele

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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 22:06:19 ; Search time 965 Seconds

(without alignments)
11071.388 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1487.2	68.4	2226	17	US-10-735-098-5 Sequence 5, Appli
3	1462.2	67.2	2262	17	US-10-735-098-7 Sequence 7, Appli
4	1454.8	66.9	2226	13	US-10-282-122A-29815 Sequence 29815, A
5	1304.8	60.0	2169	17	US-10-735-098-3 Sequence 3, Appli
6	1296.2	59.6	2124	17	US-10-735-098-9 Sequence 9, Appli
7	678.6	31.2	1000	17	US-10-343-561-15 Sequence 15, Appli
8	174.2	8.0	3300	17	US-10-467-534-80 Sequence 80, Appli
c 9	81.6	3.8	31124	13	US-10-087-192-463 Sequence 463, App
c 10	80.2	3.7	374849	13	US-10-087-192-1627 Sequence 1627, App
c 11	79.4	3.7	54786	12	US-10-052-482-211 Sequence 211, App
c 12	78.2	3.6	635	13	US-10-027-632-269927 Sequence 269927,
c 13	78.2	3.6	635	16	US-10-027-632-269927 Sequence 269927,
c 14	78	3.6	305	9	US-09-864-761-19262 Sequence 19262, A

c 15	78	3.6	496	9	US-09-864-761-2534 Sequence 2534, Ap
c 16	75.6	3.5	276	9	US-09-864-761-20595 Sequence 20595, A
c 17	75.6	3.5	193853	13	US-10-087-192-1663 Sequence 1663, Ap
c 18	75	3.4	37263	13	US-10-087-192-49 Sequence 49, Appl
c 19	73.6	3.4	554	14	US-10-101-487-69 Sequence 69, Appl
c 20	73.6	3.4	554	14	US-10-101-487-106 Sequence 106, App
c 21	73.4	3.4	96596	12	US-10-052-482-70 Sequence 70, Appl
c 22	72.8	3.3	39443	16	US-10-085-117-313 Sequence 313, App
c 23	72.2	3.3	522	14	US-10-101-487-71 Sequence 71, Appl
c 24	72.2	3.3	530	14	US-10-101-487-73 Sequence 73, Appl
c 25	72.2	3.3	122859	13	US-10-087-192-37 Sequence 37, Appl
c 26	72	3.3	2052	17	US-10-467-534-85 Sequence 85, Appl
c 27	71.4	3.3	511	13	US-10-027-632-302235 Sequence 302235,
c 28	71.4	3.3	511	16	US-10-027-632-302235 Sequence 302235,
c 29	71.4	3.3	927	16	US-10-369-493-26106 Sequence 26106, A
c 30	71.4	3.3	1032	16	US-10-369-493-26107 Sequence 26107, A
c 31	71.4	3.3	48652	13	US-10-087-192-859 Sequence 859, App
c 32	71.2	3.3	462	9	US-09-864-761-3829 Sequence 3829, Ap
c 33	71	3.3	536	15	US-10-029-386-19974 Sequence 19974, A
c 34	71	3.3	599	15	US-10-029-386-6243 Sequence 6243, Ap
c 35	71	3.3	2232	15	US-10-087-464-45 Sequence 45, Appl
c 36	70.8	3.3	58909	13	US-10-672-787-30 Sequence 30, Appl
c 37	70.6	3.2	49753	13	US-10-087-192-1855 Sequence 1855, Ap
c 38	70.4	3.2	96597	12	US-10-052-482-103 Sequence 103, App
c 39	69.6	3.2	33454	13	US-10-087-192-1111 Sequence 1111, Ap
c 40	69.6	3.2	96595	12	US-09-997-722-43 Sequence 43, Appl
c 41	69.4	3.2	438	9	US-09-864-761-4988 Sequence 4988, Ap
c 42	69.4	3.2	32069	15	US-10-004-113-7 Sequence 7, Appli
c 43	69.4	3.2	202251	13	US-10-087-192-985 Sequence 985, App
c 44	69.2	3.2	929	13	US-10-294-934-14 Sequence 14, Appl
c 45	69.2	3.2	1001	13	US-10-294-934-439 Sequence 439, App

ALIGNMENTS

RESULT 1
US-10-735-098-1
; Sequence 1, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 1
; LENGTH: 2277
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain BNCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(2274)
US-10-735-098-1

Query Match 100.0%; Score 2175; DB 17; Length 2277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTAACCGAATATGCGGCATGTGCTTTGTCCTTACTTTTGGCATCTTTGATC 60
DB 100 ATGTGTAACCGAATATGCGGCATGTGCTTTGTCCTTACTTTTGGCATCTTTGATC 159

applicants

RESULT 2

US-10-735-098-5
; Sequence 5, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain H44/76
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2223)

US-10-735-098-5
Query Match 68.4%; Score 1487.2; DB 17; Length 2226;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 1856; Conservative 0; Mismatches 298; Indels 90; Gaps 10;

Qy	1	ATGTGTAAACCGAATATGCGGCATCTCTTTGTCCTTACTTTTGGCATCTTGATC	60
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Qy	61	GGCGCAATTTGCGGTGAGCTTGTGTGAAATCAAGCGGACCGGTACCCGTCAC	120
Db	61	GGCGCAATTTGCGGTGAGCTTGTGTGAAATCAAGCGGACCGGTACCCGTCAC	120
Qy	121	TTCAAGTCTAAGAGCTTCCCACTCCGCTCGGTGCGCAATGCGCTGTTGAGGCGGATTTTCGCA	180
Db	121	TTCAAGTCTAAGAGCTTCCCACTCCGCTCGGTGCGCAATGCGCTGTTGAGGCGGATTTTCGCA	180
Qy	181	GT-----CAACCGGCCCCGCTCGGTGCGCAATGCGCTGTTGAGGCGGATTTTCGCA	240
Db	181	GTGCGGTCAACCGGCCCCGCTCGGTGCGCAATGCGCTGTTGAGGCGGATTTTCGCA	240
Qy	235	TTTCATCGTGAAGTGGACGGAAATTCGAATAGCAACAGCAGAGAAAGCTGTGC	294
Db	241	ACTTCTGATAGTGTGGCAATGATTTTCAATATAGCAACAGCAGAGAAAGCTGTGC	300
Qy	295	TTTCAAGAGGTGATGTTCTGTTTTATACGGTTCAAGAGAAATAAATCTTCAACACT	354
Db	301	TTTAAAGAGGTGATGTTCTGTTTTATACGGTTCAAGAGAAATAAATCTTCAAGTGT	360
Qy	355	AAAAGCGAAATTCATAACCGTGAATCCGATGTAGAAATTTAGACATTCAGAAAGGAAAT	414
Db	361	AAGGATAAATTCATCAACGCAATCTAATGTAGAAATTTAGACATTCAGAAATGAAAT	420
Qy	415	AAAAATATGATTAATAATTTAGATGAGGTATGATATA-----TGTAAGGGAAGAT	471
Db	421	AAAAATATGATTTATGAATTTGTGATGCGGTATGATATACTATAAAGCGAACAGAT	480
Qy	472	GAAATTAAGTGACTTCAGATTCAGAGCTTTTCCACCGCTTAGTTATGACGGTTTT	531
Db	481	GAAATTAAGTGACTTCAGATTCAGAGCTTTTCTAAATCGTTTGTGGTACGACGGTTTT	540
Qy	532	GTATATTAATTCGGGAGAACGCTCTTCCCAATCTTTACCGAGTGGCGGAACGGTGAATAT	591
Db	541	GTATATTAATTCGGGAGAACATCTTCTCCCAATCTTTACCGAGTGGCGGAACGGTGAATAT	600

Qy	592	TCTGTTAACTGGCAATATATGACCGATGCCAAACGTCTATCGAGCAGGTAAAGC---	648
Db	601	TCCGTTAACTGGCAATATATGACCGATGCCATAGTCTATCGAAAGGAAAGCAGGAGAT	660
Qy	649	GGCATTGACAATTTGGGTATTACACATTTTATCGTAAACGATGTGTGCACTTCTTAT	708
Db	661	CCTAGCGAAGATTTGGGTATTCTCGTTTATTACGGTCAAAATGTTCGAGCAACTTCTTAT	720
Qy	709	CGCGTTAAGATGTGACGAAAGGAAACATCTCTAAATATACGTTAGATTTTCGT	768
Db	721	GCTCGCACTGCCGACGACCGGAGGGAACATCTCGCGAATATACGGTTGATTTTCGAT	780
Qy	769	AACAAAACCTGTACGCGGAGCTGATTAAACCAATATGT---CAAAACCCAGTGAGAAG	825
Db	781	AAGAAACTTTGACGGTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCCATGAA	840
Qy	826	CAAAAACCGGTGACCATTTTCAACATCACTCCGATTTAAACGGCAACCGTTTACCGGC	885
Db	841	AAGAAACCACTGACCATTTTACGACATTACGCAACATTTGGACGGCAACCGCTTTACCGC	900
Qy	886	AGTGCAGAGTCAATCTCTGATTTAGCGAAAGCCATGCCAATAGGAGCATTTGTTTTTC	945
Db	901	AGTGCAGAGTAAACCGGAGTTGAAGACGAGCCACGCTGATAAGAGCATTTGTTTTTC	960
Qy	946	CATGCCGATCCGATCAGCGGCTTGAGGGCGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1005
Db	961	CATACCGATCCGATCAGCGGCTTGAGGGCGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1020
Qy	1006	GCCGACGGTTTTATCAGCAACGACAAACGATTTGGGTATTTCGAGGCAAAACA-----	1061
Db	1021	GCCGACGGTTTTATCAGCAACGACAAACGATTTTCGGCGTATTTCGAGGCAAAACA	1080
Qy	1062	-----AAATAGCCCCGCTGCGCTCTGGAACGATGGAACACACACCAAAATC	1098
Db	1081	AACGATCAAAACGACGAGATACAAATCCTGATGCGCTCTGGAACACACCAAAATC	1140
Qy	1099	TTGATTTCTGTAAATTTCCGTTGATGAGGCAAGTGTGAAATCCCGACGCGTTTGC	1158
Db	1141	TTGATTTCTGTAAATTTCCGTTGATGAGGCGGAGATAAATGCGCGCGTTTGC	1200
Qy	1159	ATTTCTCTATGCGCGATTTTGGTATCCCGCAAACTTTTGTGCAAGGGGATGAAAT	1218
Db	1201	ATTTCCCTCTGCGCGATTTTGGCATCCGCAAACTCTTGTGCAAGGGGCTGAAAT	1260
Qy	1219	CTTTGGTTAGCAGAAACCATCGAGCTTCCGACGCGCAGGAAATGACCGTCACT	1278
Db	1261	CTTTGGTTAGCAGAAACCATCGAGCTTCCGACGCGGAGAAATGACCGTCACT	1320
Qy	1279	GCTTGTTCGACTTTTTCACCTATGTGAACTTCGACCGGATAAAGAAACCGAAACCGCCG	1338
Db	1321	GCTTGTTCGACTTTTTCGACTATGTGAACTTCGACCGGATAAAGAACTGACCGCCAGCA	1380
Qy	1339	GCAAAACCGAAGGC-----GCAGACGAAGAGGATTCGGAATTGATTAATGGC	1386
Db	1381	AGTAAACCAAGGCGGAAGATAAAGGGAAGGATGAAGAGGATACAGGCTTGTGTAACGAC	1440
Qy	1387	GAAGAAAGC---GAAGACGAATCGCGATGAAGAGGAGCAGCGAGAGATGACCGCA	1443
Db	1441	GAAGAAAGCAGGAAGATGAAGCGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1500
Qy	1444	GGAGATGAAGGCGGAGGAAGACGAAGCCACAGAAAAACGAAGACGGCGGAAGACGAA	1503
Db	1501	GATGAAGAGGAGGAGGCGGAGACGAAGCCGAGAAACGAAGAGGCGGCGGAGAGACGAA	1560
Qy	1504	GCTGAAGAACCT-----GAAGAAGATCTCGCGCAGAGGCAAC---GGCAGTTCA	1551
Db	1561	GCTGAAGAACCTGAAGAACCCGGAAGAAATCGCGCGCAGAGGCGCGGTGTTGTTCA	1620
Qy	1552	AACGCACTCTGCTGTCGCGAAGCCTTAAGGACGGGATATCGACTTTTCTGAA	1611
Db	1621	GACGCGATCTGCTGCGCGCTCCGGAAGCTCTTAAGGACGGGATATCGACTTTTCTGAA	1680


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QY 1612 GGTATCGCACGGCAGAAAAGAAATATTCGCAAACTGGAGAAGCACGCTATACGGCACT 1671
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QY 1672 TGGGAAGCGGATATCGGCAAAACCAATTCATATGGGACAAATCATCGGATATAAGAGCGGCA 1731
Db 1741 TGGGAAGCGGATATCAGCAAAACCAATTCATATGGGACAAATCATCGGATATAAGAGCGGCA 1800
QY 1732 AAAGCAGTATTTACCGTGTGATTTTCGCAAGAAATCGAATTCGCGAAGCGCTGACGGAGAAA 1791
Db 1801 AAAGCAGATTTGACGTTGATTTTCGCGGAGAAATCGAATTTCCGGAACGCTGACGGAGAAA 1860
QY 1792 AACGGTGTAGAACCTCTTTCCTGATTTGAAAACGGCGTGATTTGAGGGCAACGGTTTCCAT 1851
Db 1861 AACGGTGTACAACTCTTTCCTCATATTTGAAAACGGCGTGATTTGAGGGCAATGGTTTCCAC 1920
QY 1852 GCGACAGCGGCACTCGGATGACGGATCGACCTTTTCGGGGCAGGGTTTCGACCAACCG 1911
Db 1921 GCGACAGCGGCACTCGGATAACGGCATCAATCTTTTCGGGAAATGATTCGACTAATCCT 1980
QY 1912 CAGATCTTCAAAGCTAATGATCTTCGTGTAGAGGAGGATTTTACGCGCCGGAAGCGGAG 1971
Db 1981 CCAAGTTTCAAAGCCAAATATCTCTGTACAGCGGCTTTTACGCGCCGCGAGCGGAG 2040
QY 1972 GAATTCGGCGGTATATTTTCAATAATGATGGGAAATCTCTTGGTATAACTGAAGGTACT 2031
Db 2041 GAATTCGGCGGTACTATTTTCAATAATGATGGGAAATCTCTTGGTATAACTGAAGGTACT 2100
QY 2032 GAAATTAAGTTGAAGCTGATGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 2091
Db 2101 GAAATTAAGCTGAAGCTGAAGTTGAAATGAAGCTGGTGT----- 2141
QY 2092 GATGTGAAACAGTTAAACCTGAAGTTAAACCCCAATTCGGCGTGGTATTCGGTGGGAAG 2151
Db 2142 --TGGCAACAGTTAAACCTGAAGCTAAACCCCAATTCGGCGTGGTATTCGGTGGGAAG 2199
QY 2152 AAAGATAATAAGAGGTGAAAAA 2175
Db 2200 AAAGATAATAAGAGGTGAAAAA 2223
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RESULT 3

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US-10-735-098-7
; Sequence 7, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M990
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2259)
US-10-735-098-7
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Query Match 67.2%; Score 1462.2; DB 17; Length 2262;
Best Local Similarity 81.1%; Pred. No. 0;


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Db 1 ATGTGTAAACCGAAATATATGCGCGCATTTGTCTTGTTCCTTACTTTTGGCATCTTGTATC 60
QY 61 GCGCGCAATTTTCGGCGTGCAGCTGTGTGCGAATCAACGCCGACCGCG----- 108
Db 61 GCGCGCAATTTTCGGCGTGCAGCTGTGTGCGAATCAACGCCGACCGCGCGCAACTCTGTCTCA 120
QY 109 TACCCCGTCACTTTCAGTCTAAGGACGTTCCCACTCCGCGCCCTGTCACCAACCTCTTATA 169
Db 121 GATTCCAATCTTCCAAATCTCTGCGGATAGCCTGCTCCAGCTCCTCGCGAGCCTTCGGTA 180
QY 169 GAAATCACGCGGTCACCGCGCCGCGTGGTGGCGCAATGCGGCTGCCAAGCGGAAT 228
Db 181 GAAATCACGCGGTCACCGCGCCGCGTGGTGGCGCAATGCGGCTGCCAAGCGGAAT 240
QY 229 ACTGCTTTTTCATCGTCAAGATGGCAGGAAATTCCAAATAGCAAAACAAGCAGAGAAAAG 288
Db 241 ATCGCAACTTTTGTATTAATAATGTAATGAAATTCCTCAATAGTAAGCGGAGAGGATAT 300
QY 289 CTGCTGTTCAAGAAAGTGATGTTCTGTTTTATACGGTTCAAAAGGAAATAAACTCAA 348
Db 301 CTGCGGCTCAAAGAGAGGATATCTCTGTTTTAGACGGTACGCGGAAAGAACAGGCTGAC 360
QY 349 CAACTTAAAGCGGAATTCATAAACGATTCGATGCGATGAGAAATTAGGACATCAGAAAAG 408
Db 361 AAACCTTAAAGGAAATCAACCGGCGCATCTTAATGCACCAATCTACACGTCGCGATTTA 420
QY 409 GAAATTAATAAATAATGATTATATAAATTTGTAGATGACAGGTTATGTATA---TGTAAAGGGA 465
Db 421 AAAGATGATCGGTATCAATATAATAATATGTCGCGCGGATATGTTTTACTAGATATGGA 480
QY 466 AAAGATGAAATTAAGTGGACCTTCAGATTAACAGCAGTTTTTCCACCGCTTAGGTTATGAC 525
Db 481 ACAGATGAAATCGAACAGAACTCAGCGGCTAAGCGGGTTACCCACGCTTAGGTTATGAC 540
QY 526 GGTGTTGTATATTTTCCGGAGAACGTCCTTCCCATCTTTACCGATCGCGGAAACGGTG 585
Db 541 GGTGTTGTATATTTTCCGGAGAACGTCCTTCCCATCTTTACCGAGTGGGAAACGGTG 600
QY 586 GAATATTTCTGTAACCTGGCAATATATGACCGATGCCCCAACGTCATCGAGCAGTAAGGCG 645
Db 601 GAATATTTCTGTTAACTGGCAATATATGACCGATGCCCCAACGTCATCGAGCAGTCAAGCG 660
QY 646 GTTGGCATGACAAATTTGGGTTATATACATTTTATGTTAAACGATTTGGTGAACCTTCT 705
Db 661 GTTGGCATGACAAATTTGGGTTATATACATTTTATGTTAAACGATTTGGTGAACCTTCT 720
QY 706 TATGCGGCTAAGGATGTCGACGAAAGGAAACATCTCTGCTAAATATACGGTAGATTTTC 765
Db 721 TATGCGGCTAAGGATGTCGACGAAAGGAAAGATCTCTGCGCAATATACGGTTGATTTT 780
QY 766 GGTAAACAAAACCTGACGCGGAGCTGATTTAAACCAATATGT-----CAAACCCAGT 819
Db 781 GATAACAAAACCATGAATGCGAAGCTGATTTAAATATCAGTATGCGGAAATTAAGAAGAT 840
QY 820 GAGAAGCAAAAACCGCTGACCAATTTACATCATCTGCGGATTTAAACCGGAAACCGCTTT 879
Db 841 GAAACCAAAAACCGCTGACCAATTTACGACATTTACTGCAAAAATTTGGACGGCAACCGCTTT 900
QY 880 ACCGCGCAGTGCCAAGTCAATCTGATTTTACGAAAGCCATGCGCAATAGGAGCATTTG 939
Db 901 ACCGCGCAGTGCCAAGTCAATCTGATTTTACGAAACCACTTTCGCGGTAATGAGCGCTTG 960
QY 940 TTTTTCATGCGGATCGCGGATCAGCGGCTTGAGGGCGGTTTTTTTCGCGCATAGGGGAA 999
Db 961 TTTTTCATGCGGATCGCGGATCAGCGGCTTGAGGGCGGTTTTTTTCGCGCATAGCGAGAA 1020
QY 1000 GAGCTTGGCGGACGGTTTATCAGCAACGCAACAGGATTTTCGGTGTATTCGAGGCAAA 1059
Db 1021 GAGCTTGGCGGACGGTTTATCAGCAACGCAACAGGATTTTCGGTGTATTCGAGGCAAA 1080
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QY	1060	CA	-----AAATAGCCCGTGCCTCTCGAAAAACACACC	1092
Db	1081	AA	AAACAGACACCAACGCAGCAGATACAAACCTGCCCTCTGGAACACACACC	1140
QY	1093	AA	AAATCTTGATCTCTGAAAAATTCCTGGTATGAGGCAAGTGGTGAATAATCCCGACCG	1152
Db	1141	AA	AAATCTTGATCTCTAAAAATTCCTGGTATGAGGCGCATGATGCCATGCGCGTAAG	1200
QY	1153	TT	TGTCATTTCTCCTATGCCCGATTTTGGTCAATCCGACAAACTCTCTGTGCAAGGGCAT	1212
Db	1201	TT	TGTCATTTCTCTATGCCCGATTTTGGTCAATCCGACAAACTCTCTGTGCAAGGGCGT	1260
QY	1213	GA	AAATCTCTTTGGTTAGCCAGAGAAACCATCGAGCTTGCCGACGGCAGGAAAAATGACC	1272
Db	1261	GA	AAATCTCTTTGGTAAACGAAGAACAAATCATCAAGCTTGCCGACGCGAGAAAAATGACC	1320
QY	1273	GT	CAGTCTTGTGCGACTTTTGTACTATGTCAAACTCGGACGGATAAAAACCGAACCG	1332
Db	1321	GT	CGTCTTGTGCGACTTTTGTACTATGTCAAACTCGGACGGATAAAAACCGATCGC	1380
QY	1333	CC	CGCCGCCAAACCCGAGGC-----GCAGGACGAAGAGGATTCGACATTGAT	1380
Db	1381	CC	CGCAGTAAACCAAGGCGGAGATAAAGGGAGATGAAGGGGTGCAGCGTTGAT	1440
QY	1381	AA	TGGCGAAGAAAGCGAAGACGAAATCGCGCATGAGAGAAAGCACCAGATGCAGCC	1440
Db	1441	AA	CACCAAGAAAGCGAAGACGAAAGCGTGTAGAGACGAAGCGCGCAAGAGACGAAC	1500
QY	1441	GC	AGAGATGAAGCACGCGAAGAGACGAAGCCAC-----AGAAAAAC	1482
Db	1501	TC	GAGAGATTAATGCGAAGACGAAGAGCAACCGCCGACGAGAACCGAGAGATT	1560
QY	1483	GA	GACCGCGAAGAAAGACGAGCTGGAAGAACCTCTGAAGAGAATCGTCGGCAGAGCAAC	1542
Db	1561	GAT	GAACCCGAGAGAGGAGGAAGTTGAAGAACCCGAGAAAAATCGCCGCGAGAGGCAAC	1620
QY	1543	GG	CAGTTCAAACGGCATCTCTGCTGTCCCGAAGCCTCTAAGCGAGGATATCGACCTT	1602
Db	1621	GG	CGTTTCAGCAGCATCTCTGCTGCCCTCTAGAAGCCTCTAAGCGAGGACATCGACCTT	1680
QY	1603	TT	CTGTAAGAGTATCCGACGCGCAGAAACCAATATCCGCAAACTGAGAGACACGCTAT	1662
Db	1681	TT	CTGTAAGAGTATCCGACGCGCAGAAACCGATATTCGCAAGCGGAAACCGCGCATAT	1740
QY	1663	AC	CGGCATCTGGGAAGCGGCTATCGGCAAAACCCCATCAATGGGCAATATGCGGATAAA	1722
Db	1741	AC	CGGCATCTGGGAAGCGGCTATCGGCAAAACCCCATCAATGGGCAATATGCGGATGAA	1800
QY	1723	GA	AGGCGCAAAAGCAGTATTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAACGCTG	1782
Db	1801	AA	AGCGGCAAAAGCAGATTTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG	1860
QY	1783	AC	GAGAAAAAACCGGTGTAGAACCTGCTTTCCGTATTTGAAAAACCGCGCTGATGAGGGCAAC	1842
Db	1861	AC	GAGCAAAACCGGTGTAGAACCTGCTTTCCATATTTGAAGACGCAAGATTTGATGGCAAC	1920
QY	1843	GG	TTTCCATGCGACAGCGCGCATCTCGGATGACGCGATCGACCTTTCGGCGAGGGTTCTG	1902
Db	1921	GG	TTTCCACGCGACAGCGCGCATCTCGGATGACGCGATCGACCTTTCGGGAAATTTGGTTCTG	1980
QY	1903	ACC	AAACCGCAGATCTTCAAAGCTAAATCATCTTCGTGTAGAAAGAGAGATTTTACGGCCCG	1962
Db	1981	ACC	GAACCCCAAAACATTCAGCTAGTAAATCTTCGTGTAGAAAGAGAGATTTTACGGCCCG	2040
QY	1963	AAG	CGGAGGAATTTGGCGGTATTTATTTTCAATATGATGGGAAATCTCTTGGTATAACT	2022
Db	2041	CA	GGCGCGGAATTTGGCGGTACTATTTTCAATATGATGGGAAATCTCTTGGTATAACT	2100
QY	2023	GA	AGTACTGAAAAATAAGTTGACGCTGATGTGATGTTGATGTTGATGTTGATGTTGAT	2082
Db	2101	GA	AAATATTTGAAATATGAGCTCAAGCTGAGTTGAGTTGAGCTGAGCTGAGCTGAGTTGAA	2160

QY 2083 GCTGATGCTGATGTTG---AACAGTTAAAC---TGAAGTTAAACCCCAATTGGCGGTG 2133
Db 2161 GTTGAAGCTGATGTTGGCAACAGTGTAGAACCTGATGAAGTTAAACACAAATTGGCGGTG 2220

QY 2137 GTATTTCGTCGCGAGAGAGATAATAAGAGCTGGA AAAA 2175
Db 2221 GTATTTCGTCGCGAGAGAGATATGCGAGAGTGGAAAAA 2259

RESULT 4
US-10-282-122A-29815
; Sequence 29815, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29815
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-282-122A-29815



Db 121 TTCAAGTCTAAGAGCGTTCCCACTTCGCCCCCTGCGGGCCTTCGGTAGAAGCAACCGCG 180
QY 181 GTCAACGGGCCCGCGTGGCGCAATCGCGTCCCAAGCGGAATACGTCTTTTCAT 240
Db 181 GTCAACGGGCCCGCGTGGCGCAATCGCGTTCGGGCTGTGAGGGCGGAATATGCTTTTCAT 240
QY 241 CGTGAAGATGGCAGCGGAATTCGAATPAGCAAAACAAGCAGAGAAAAGCTGTCTGTTCAA 300
Db 241 CGTGAAGATGGCAGCGGAATTCGGATAGCAAAACAAGCAGAGAAAAGCTGTCTGTTCAA 300
QY 301 GAAGGTGATGCTCTGTTTATACGGTTCGAAGGAATTAACCTTCAACAACTTAAAGC 360
Db 301 GAAGGTGATGCTCTGTTTATACGGTTCGAAGGAATTAACCTTCAACAACTTAAAGC 360
QY 361 GAAATTCATAAAGCGTGATTCGGATGTAGAAAATAGGACATCAGAAAAGGAAAAATAAAAA 420
Db 361 AAAATTCATAAAGCGTATTCGAATGTAGAAAATAGGACATCAGAAAATGAAAATAAAAA 420
QY 421 TATGATTAATAATTTGTAGATGACGGTTATGTATATACTACAAAAGGAAAAAGATGAAAT 477
Db 421 TATGTTATGAATTTGTAGATGACGGTTATGTATATACTACAAAAGGAAAAAGATGAAAT 480
QY 478 AAGTGGACTTCAGATTAACAGCAGTTTCCAAACCGCTTAGGTTATGACGGTTTGTATAT 537
Db 481 GAGTGGACTTCMAATCACAAGCAGTTTACCTACCGGTTTGGTTATGACGGTTTGTATAT 540
QY 538 TATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGGAACGGTGGAAATATCTGGT 597
Db 541 TATTCGGAGAACATCTTTCGAATCTTTACCGAGCGCGGGAACGGTGGAAATATCTGGC 600
QY 598 AACTGGCAATATATGACCGATGCCAAACGGTCAATCGAGCAGGTAAAGC---GGTTGCAATT 654
Db 601 AACTGGCAATATATGACCGATGCCAATCGTCAATCGAACAAGGAAAAAGCAGAGATCCTAG 660
QY 655 GACAATTTGGTTTATTAACATTTATGTTAGTAAAGTGTGGTCACTTCTTATGCGCT 714
Db 661 GAAGATTTGGTTTATATCGTTTATACGGTCAAAATGTTCGGAGCAATCTTATGCTGG 720
QY 715 AAGGATGTGACGAAAGGAAAAACAATCCTGTCTAAATATACGGTAGATTTTCGGTAACAAA 774
Db 721 ACTGCCGACGACCGAGAGGAAAAACATCCTGCCGATATACGGTAGATTTTCGGTAGAAA 780
QY 775 ACCGTGACGGGAGCTGATTAATAAACCAATATGT---CAAAACCGAGTGAAGAGCAAAA 831
Db 781 ACTTTGACGGGTAAATTAATAAAATCAGTATGTGCAAAAAGAAAACCGATGAAAAGAAA 840
QY 832 CGCTGACCAATTTACAACATCACTGCCGATTTAAACGGCAACCGCTTACCGCGAGTGC 891
Db 841 CGCTGACCAATTTACGATTTACTGCAATTTGCAATTTGAGCGGCAACCGCTTTACCGG 900
QY 892 AAGGTCAATCTGATTTAGCAAAAAGCCATGCCAATAAGGAGCATTTGTTTTTCCATGCC 951
Db 901 AAAAGTTAACACCGAGTGAAGACGAAACACGCTGATATAAGACATTTGTTTTTCCATACC 960
QY 952 GATGCCGATCAGCGCTTCAGCGCGTTCCTGCGGATTAAGGGGAAGAGCTTCGCGGA 1011
Db 961 GATGCCGATCAGCGCTTCAGCGCGTTCCTGCGGATTAAGGGGAAGAGCTTCGCGGA 1020
QY 1012 CGGTTTATCAGCAACGACACGCGTATTCGGTGTATTCGAGGCAAAACAAAATAGCCCC 1071
Db 1021 CGGTTTATCAGCAACGACACGCGTATTCGGGCTATTCGAGGCAAAACAAAACAGAC 1080
QY 1072 G-----TCCGCTCTGAAAAACACACCAAAATCTTG 1101
Db 1081 GCATCAAAAGCGATCAGATCAAAATCCTGCTATGCGCTCTGAAAAACACACCAAAATCTTG 1140
QY 1102 GATTCCTCTGAAATTTCCGTTGATGAGCAAGTGTGAATTCCTCCGACCGTTTGGCATT 1161
Db 1141 GATTCCTCTGAAATTTCCGTTGATGAGCAAGTGTGAATTCCTCCGACCGTTTGGCATT 1200
QY 1162 TCTCCTATGCCGATTTTGGTTCATCCGACAACTTCTTGTGCAAGGCGATGAAATTCCT 1221
Db 1201 TCCCTATGCCGATTTTGGTTCATCCGACAACTTCTTGTGCAAGGCGGTGAATTCCTC 1260

RESULT 5

US-10-735-098-3

; Sequence 3, Application US/10735098

QY 1222 TTGGTTAGCCACAGAGAAAAACCATCGAGCTTCCGACGCGCAGGAAAAATGACCGTCAAGTCT 1281
Db 1261 TTGCTCAAGATACTCAACCATCATGATCTTCCGACGCGCAGGAAAAATGACCGTCAAGTCT 1320
QY 1282 TGTTCGACATTTTTCGCTTATGTGAAACTCGGACGATAAAAACCGAACCCCGCGCGCC 1341
Db 1321 TGTTCGACATTTTTCGCTTATGTGAAACTCGGACGATAAAAACCGAACCCCGCGCGCAAGT 1380
QY 1342 AAACCGACGCGCAGACGAGAGA---GGATTCCGACATTTGATTAATGGCAGAAAGCGGAA 1398
Db 1381 AAACCGAAGCGCGAAGATGAAAAATCCGAAGATGAAATTTGGTGAAGACCGAGGAAAAATGAA 1440
QY 1399 GACCAATCGCGCATGAAGAAGAACCCAGGAAGTGCAGCCGACGAGATGAAGCAGC 1458
Db 1441 GAGGATTTGGTCTCTGAGAGAGAAAACACGGAAGACGAAGTCTGTAAGATGAAGACGA 1500
QY 1459 GAAGAAGACGAAGCCACAGAAAAAC----- 1482
Db 1501 GAAGAAGACGAAGTTCGGAAGATGCTAAACAGTGAAGACGAAGAAATCGCCGAAGAA 1560
QY 1483 -----GAAGACGGCGAAGACGAGCTGAAGAACTTGAAGAAATCTGTCGGCAGAA 1536
Db 1561 GATGATGATGAAGCCGAAGAGGAGGAAGTTGAAGAACCCGGAAGAAATCGCCGGAAGAA 1620
QY 1537 GGCACAC---GGCAGTTTCAAAACGCCATCTCTGCTCTCCCGAAGCCTCTAAAGGCAGGAT 1593
Db 1621 GCGCGCGGTGGCGTTTACAGCGCATCCCGCGCTTCGAGAGCCCTTAAGACAGGAC 1680
QY 1594 ATCGACCTTTTCTGAAAGGTATCCGACGGCAGAAACGAATATTCGCAAACTGGAGAA 1653
Db 1681 ATCGACCTTTTCTGAAAGGTATCCGACGGCGGAAGCGACATTCGCAAACTGGAGAA 1740
QY 1654 GACGCTATACCGGCACCTTGGGAAGCGGTATCGGCAAAACCCATTCATATGGGACATCAT 1713
Db 1741 GCACGCTATACCGGCACCTTGGGAAGCGGTATCGGAAAGCGGTATCAGCAAAACCCATTCATATGGGTAATAAG 1800
QY 1714 GCGGATAAAGAAAGCGGCAAAAGCAGTATTTACCGTTGATTTTCGGCAAGAAATCGATTTCC 1773
Db 1801 GCGGATAAAGAAAGCGGCAAAAGCAGATTTGAGTTGATTTTCGGCAAGAAATCGATTTCC 1860
QY 1774 GGAACGCTGACGAGGAAAAACCGGTGTAGAACCTGCTTTCCGTTATGAAAACCGCGTGATT 1833
Db 1861 GGAACGCTGACGAGAAAAACCGGTGTAGAAAGCTGCTTTCTATATTTGAAAAGGTGTGATT 1920
QY 1834 GAGGCAACGGTTTCCATGCGACAGCGCACCTCGGGATGACGGATCGACCTTTCCGGG 1893
Db 1921 GATGGCAACGGTTTCCACGCGACACGCACTCGGGATAACGGCATCAATCTTTTCGGGA 1980
QY 1894 CAGGGTTTCGACCAAAACCGCAGATCTTCAAAGCTAATGATCTTTCGCTAGAAGGAGATTT 1953
Db 1981 AATGGTTCCGACCAACCCCAAAACCTTCCAAAGCTAGTGAATCTTCGCTGTAAGAGGATTT 2040
QY 1954 TACGGCCGGAAGCGGAGGAAATGGCGGTATTAATTTCAATAATGATGGGAAAAATCTCTT 2013
Db 2041 TACGGCCGCGAGCGGAGGAAATGGCGGTACTATTTTCAAAGATGGGAAATCTCTT 2100
QY 2014 GGTATAACTGAAGGTACTGMAAATAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTT 2073
Db 2101 GATATACTGAAGATATTGACAAATGAAATTTGAAGCTGA----- 2138
QY 2074 GATGTTGATGCTGATGCTGATTTGAACAGTTTAAACCTGAAAGTTAAACCCCAATTCGGC 2133
Db 2139 -----TGCTGGCGAACAGTTTAGAACCTGAAAGTTAAACCCCAATTCGGC 2181
QY 2134 GTGCTATTTCGGTGCAGAGAAAGATTAATAAGAGGTGGAAAAA 2175
Db 2182 GTGCTATTTCGGTGCAGAAAAAGATATGAGGAGGTGGAAAAA 2223

Publication No: US20040131634A1
GENERAL INFORMATION:
APPLICANT: Pettersson-Fernholm, Annika Margareta
APPLICANT: Tomassen, Johannes Petrus Maria
TITLE OF INVENTION: Neisseria lactoferrin Binding Protein
FILE REFERENCE: B45106C1
CURRENT APPLICATION NUMBER: US/10/735,098
CURRENT FILING DATE: 2003-12-12
PRIOR APPLICATION NUMBER: 09/485,760
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: PCT/EP98/05117
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: GB 9717423.9
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: GB 9805544.8
PRIOR FILING DATE: 1998-02-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2169
TYPE: DNA
ORGANISM: Neisseria meningitidis strain M981
FEATURE:
NAME/KEY: CDS
LOCATION: (1)....(2166)
US-10-735-098-3

Query Match 60.0%; Score 1304.8; DB 17; Length 2169;
Best Local Similarity 79.1%; Pred. No. 9e-300;
Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;

QY	1	ATGTGTAACACCGAATTATGCGGCATGTCCTGCTGGCCTTACTTTGGCACTTGTATC	60
DB	1	ATGTGTAACCGAATTATGCGGCATGTCCTGCTGGCCTTACTTTGGCACTTGCATC	60
QY	61	GGCGCAATTCGGGTGAGCCTGTTGCAATCAACGCGACCGCTACCCCGTCACT	120
DB	61	GGCGCAATTCGGGTGAGCCTGTTGCAATCAACGCGACCGCTACCCCGTCACT	120
QY	121	TTCAAGTCTAAGACGCTTCCACTCGCCCTCGCCAAACCTTCTATAGAAATCAGCCG	180
DB	121	TTCAAGTCTAAGACGCTTCCACTCGCCCTCGCCAAACCTTCTATAGAAATCAGCCG	180
QY	181	GTCAACCGCCCGCTGCGTGGCAATCGGCTGCCAAGCGGGAATCTGCTTTTCAT	240
DB	181	GTCAACCGCCCGCTGCGTGGCAATCGGCTGCCAAGCGGGAATCTGCTTTTCAT	240
QY	241	CGTGAAGATGCGCGGAATTCGAATAGCAACACGACGAGAAAGCTGTGTTTCAA	300
DB	241	CGTGAAGATGCGCGCAATTCGCGATAGCAACACGACGAGAAAGCTGTGTTTAAA	300
QY	301	GAAGTGTATGTCGTTTTATACGGTTCAAAGAAATTAACCTTCAACAACTTAAAGC	360
DB	301	GAAGTGTATGTCGTTTTATACGGTTCAAAGAAATTAACCTTCAACAACTTAAAGC	360
QY	361	GAAATTCATAACGTGATTCGATGTGAAATTAGCATCAGAAAGGAAATTAATAAA	420
DB	361	GAAATTCATAAAGTAACTCTGAGCAAGCATTAACCAATCGAAATTAATAAA	420
QY	421	TATGATTAATAATTGTAGATCGAGTTATCTAT---ATGTAAAGGAAAGATGAAT	477
DB	421	TATTAATATCGTTTGTGTCGCTGATGTTGTTTCTAATAAACGGAAGATGAAT	480
QY	478	AAGTGGATCTCAGATTACAAGCAGTTTCCAAACCGCTTAGGTATGACGGTTTGTATAT	537
DB	481	GAGAAACATTCGATGAAGACGATTTCTAATCTTTAGCTATGACGGTTTGTATAT	540
QY	538	TATTCGGGAGACGTCCTTCCCAATCTTTACGAGTGGGGAACGGTGAATATTTCTG	597
DB	541	TATCTCGGGAACATCTTCCCAATCTTTACGAGCGGGGAACGGTGAATATTTCCGC	600
QY	598	AACTGGCAATATATGACCGATGCCAAACGTATCGAGCAGGTAAAGCGGTGGCAATGAC	657

DB	601	AACTGGCAATATATGACCGATGCGCATACGTATCGGAGAGGTAAAGGGTTTCCAGTGTG	660
QY	658	AAATTTGGTTTATACACATTTTATGGTAAACGATGTTGGTCAACTTCTTATGGGCTAAG	717
DB	661	GAATTTGGTTTATACACATATATGGTAAATGGGAGCTTCTTATGAGCTAGG	720
QY	718	GATGTCGAGAAAGGAAACATCTCTGCTAAATATACGTTAGATTTTCGGTAAACAAACC	777
DB	721	GATGCGGATGCGCGGAAACATCTCTGCGCAATATACGTTAAATTCGACAAACAAAC	780
QY	778	CTGACGGCGGAGCTGATTTAAACCAATATCTCAAAACCCAGTGAGAAGC---AAAAACCG	834
DB	781	CTGGAAGGTAAAGTTGATTTAAATAATCAGTATGTGCAAAAGAGATGATCTCTAAATCCA	840
QY	835	CTGACCAATTTACACATCACTGCGGATTTAAACGGCAACCGCTTTACCGGAGTCCCAAG	894
DB	841	CTGACCAATTTACACATTTACCGCAATTTGGACGCGCAACCGCTTTACCGGAGTCCCAA	900
QY	895	GTCAATCTCTGATTTAGCGAAAGCCATGCCAATAAGGAGCATTTGTTTTCATCCCGAT	954
DB	901	GTTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATATTTGTTTTCATACCGAT	960
QY	955	GCGGATCAGCGCTTTGAGGCGGTTTTCGCGGATTAAGGGGAAAGAGCTTCCCGAGCG	1014
DB	961	GCGGATCAGCGCTTTGAGGCGGTTTTCGCGGATTAAGGGGAAAGAGCTTCCCGGCGG	1020
QY	1015	TTTATCAGCAACGACAAACAGCGTATTCGTTGATTTTCGACGGCAACAA-----1061	
DB	1021	TTTATCAGTAAAGCAACACGCGTATTCGCGGTGTTTCGAGGCAACAAACAAACAGACA	1080
QY	1062	-----AAATAGCCCGTGGCGTCTGGAAAAACACACCAAAATCTTGGAT	1104
DB	1081	GCAAACGATCAGATACAAAATCTGCGCTTCTGGAAAAACACCAAAATCTTGGAT	1140
QY	1105	TCCTGAAATTTTCGTTGATGAGCAAGTGGTAAATCCCGACCGTTTTCATTTCT	1164
DB	1141	TCCTGAAATTTTCGTTGACGAGGCGACTGATGACCTGCGGTAAGTTTGCATTTCC	1200
QY	1165	CTATCCCGATTTTGTCTATCCGACAACTTCTTGTGAAAGGCGATGAAATTCCTTTG	1224
DB	1201	ACTATGCCGATTTTGTCTATCCGACAACTTCTTGTGAAAGGCGTGAATTCCTTTG	1260
QY	1225	GTTAGCCAAAGAAAAACCATTCGAGCTTCGCGACGCAAGAAATGACCTGAGTCTGT	1284
DB	1261	GTTAGCCAAAGAAAAACCATTCGAGCTTCGCGACGCGCAAGAAATGACCTGAGTCTGT	1320
QY	1285	TGCGACTTTTGTACCTATGTGAACTCGGACGATATAAAACCGCCCGCGCCGCAAA	1344
DB	1321	TGCGATTTTCTGACCTATGTGAACTCGGACGATATAAAACCGCCCGCGCCGCAAA	1380
QY	1345	CCGAAGCGCAGGACGAGAGGATTCGACATTTGATTAATGCGCAAGAAAGCAAGACGAA	1404
DB	1381	CCGAAGCGCAGGATGAGAGGATTCGACATTTGATTAATGCGCAAGAAAGCAAGACGAA	1440
QY	1405	ATCGCGGATGAAGAAAGGACCGCAAGATGCGCCGACGAGATGAGGACGAGAGAA	1464
DB	1441	ATTTCCGAAGATGATAACGCGCAAGATGAAGTCAACGAAGAGAGGAGCTGAAGAAACC	1500
QY	1465	GACGAAGCCACAGAAACCGAGACGCGCAAGAA-----1497	
DB	1501	GAAGAAGAACTGATGAGACGAGAGAGAAACCCGCAAGAACTGAAGAACTGAAGAA	1560
QY	1498	-----GACGAAGCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA	1542
DB	1561	ACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA	1620
QY	1543	GGCGATTTCAAACGCCATCTGCTGTCGGAAGCTCTTAAGGACGAGATATCGACCTT	1602
DB	1621	GCGGTTTCCAGGACGATCTCTGCCACTCCGGAAGCTCTAAAGGACGAGATATCGACCTT	1680
QY	1603	TTCTGAAAGATATCCGCAACGCGCAAGACGATATTCGCAAACTGGAAGAGACGCTAT	1662
DB	1681	TTCTGAAAGATATCCGCAACGCGCAAGACGCTATTCGCAAACTGGAAGAGACGCTAT	1740

QY 1663 ACCGGACCTTGGAGCGGTATCGGCAAAACCAATCAATGGACCAATCATGCGGAT--- 1719
Db |||||
QY 1741 ACCGGACCTTGGAGCGGTATCGGCGTCCGGAATAAGAAAGCGCAACAGCTAGATGGC 1800
Db |||||
QY 1720 ----- 1860
Db |||||
QY 1801 ACTACGTCATTCAAAGGATAGCTATGCGAATCAAGCGGCAAAAGCAAAATTTGACGTT 1860
Db |||||
QY 1750 GATTTCCGCAAGAAATCGATTTCCGGAACGCTGACGGAAGAAACGGGTAGAACCTGCT 1809
Db |||||
QY 1861 GATTTTGGTGCAGCTCGCTTTTCAGTAAGTTGACAGAAATAATGATACACACCCCGCT 1920
Db |||||
QY 1810 TTCCTGATGAAACCGCGTGTATGAGGCAACGCTTCCATGCGACACGCGGCACTCGG 1869
Db |||||
QY 1921 TTTTATATGAAAAAGGTGTGATGATGCAACGCTTCCACGCTTTGCGCGTACTCGT 1980
Db |||||
QY 1870 GATGACGCGATCGACCTTTCCGCGCAGGCTTCGACCAACCGCAGATCTTCAAAGCTAAT 1929
Db |||||
QY 1981 GAAAAATGCTGTGATTTGCTCGGCAAGCTTCGACATAATCCCAAAGTTTAAAGCCAGT 2040
Db |||||
QY 1930 GATCTTCGTAGAAAGGAGATTTTACGCCCGCAAGGCGGAGAAATTCGGCGGTATATT 1989
Db |||||
QY 2041 AATCTTCTCGTAGAAGGAGGATTTTATGGTCCGCGAGGCGGAGAGCTTGGTGGTATATT 2100
Db |||||
QY 1990 TTCAATATGATGGGAA 2007
Db |||||
QY 2101 ATCGACAGTACCGGAAA 2118
Db |||||

RESULT 6

US-10-735-098-9
; Sequence 9, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain 881607
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2121)
US-10-735-098-9

Query Match 59.6%; Score 1296.2; DB 17; Length 2124;
Best Local Similarity 79.0%; Pred. No. 9.9e-298;
Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;
QY 1 ATGTGTAAACCGAATATATGGCGGATGTCTTGTGGCTTACTTTTGGCATCTTGATC 60
Db 1 ATGTGTAAACCGAATATATGGCGGATGTCTTGTGGCTTACTTTTGGCATCTTGATC 60
QY 61 GCGCGCAATTTCCGGGTGAGAGCTTCTGCGAATCAAGCGGACCGGATACCCCGTACT 120
Db 61 GCGCGCAATTTCCGGGTGAGAGCTTCTGCGAATCAAGCGGACCGGATACCCCGTACT 120
QY 121 TTCAAGTCTAAGGAGCTTCCCACTCCGCCCTCCCAACCTTCTATAGAAATCATCGCG 180

Db |||||
QY 121 TTCAAGTCTAAGGAGCTTCCCACTCCGCCCTCCCAACCTTCTATAGAAATCATCGCG 180
QY |||||
Db 181 GTCAACCGCCCGCGCTCGGTGCGCAATGCGGCTGCCAAGGCGGAATCTGCTTTTCAT 240
QY |||||
Db 181 GTCAACCGCCCGCGCTCGGTGCGCAATGCGGCTGCCAAGGCGGAATCTGCAACTTCT 240
QY |||||
Db 241 CGTGAAGATGGCAGCGAATTCCAATAGCAACCAAGCAGAGAAAGCTGCTGTTTCAA 300
QY |||||
Db 241 GATAAGGATGGCAATGATTTTCCAAATAGCAACCAAGCAGAGAAAGCTGCTGTTTAA 300
QY |||||
QY 301 GAAAGTGTATGTTCTCTGTTTTTATACGTTCCAAAGGAAATAAATCTTCAACAACTTAAAGC 360
QY |||||
Db 301 GAGGAGATATCCCTGTTTTTATACGTTCCAAAGGAAATAAATCTTCAACAACTTAAAGC 360
QY |||||
QY 361 GAAATTCATAACGCTGATTCGATGTAGAAATTAGCAATCAGAAAGGAAATAAATAA 420
QY |||||
Db 361 AAAATTCGTCAACCAATCTTACGCAAGCATTCACCATCGAAAGAAATAAATAA 420
QY |||||
QY 421 TATGATTAATAATTTGTAGATGACAGTTTATGTATTA---TGTAAGGAAAGATGAAAT 477
QY |||||
Db 421 TATGATTAATAATTTGTAGATGACAGTTTATGTATTAATAAGACGAAAGATGAAAT 480
QY |||||
QY 478 AAGTGGACTTCAGATTACAAGCAGTTTCCAAACGCTTAGGTATGACGGTTTGTATAT 537
QY |||||
Db 481 GAGTGGACTTCCAAATTAACAAGCTTACCAACCGTTTGGTTATGACGGTTTGTATAT 540
QY |||||
QY 538 TATTCGGAGAACGCTTCCCAATCTTTACCGAGTCCGGGAAACGGTGAATATTCGTG 597
QY |||||
Db 541 TATTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGAATATTCGGC 600
QY |||||
QY 598 AACTGGCAATATATGACCGATGCCAAAGCTCATCGAGAGTAAGGC---GGTTGGCAT 654
QY |||||
Db 601 AACTGGCAATATATGACCGATGCCAAAGCTCATCGAGAGTAAGGC---GGTTGGCAT 660
QY |||||
QY 655 GACAAATTTGGTTTATACACATTTTATGTTAAACCATATGTCAAACCCAGTGAGAGC---AAAA 831
QY |||||
Db 781 ACTCTGAATGGCAAGCTGATTAATAATTCAGTATGTGCAAAAGAGAGATGATCTCTAA 840
QY |||||
QY 832 CCGCTGACCAATTTACAACATCACTGCGGATTTAAACGGCAACCGCTTACCGGAGTGCC 891
QY |||||
Db 841 CCACTGACCAATTTACGACATTTACTGCAAAATTTGGACGGCAACCGCTTACCGGAGTGCC 900
QY |||||
QY 892 AAGTCAATCTGATTTAGCGAAACCATGCGCAATAGGAGCATTTGTTTTTCCATGCC 951
QY |||||
Db 901 AAAGTTAACACAGAGGTGAAGACGAATCAGCTGTATAAGAAATATTTGTTTTCCATACC 960
QY |||||
QY 952 GATCGGATCAGCGCTTCAGGCGGCTTTTTCGGCGATAGGGGAGAGCTTGCGGA 1011
QY |||||
Db 961 GATCGGATCAGCGCTTCAGGCGGCTTTTTCGGCGATAGGGGAGAGCTTGCGGA 1020
QY |||||
QY 1012 CCGTTTATCAGCAACGACAAAGCTGATTCGGTGTATTCGAGGCAACCA--- 1061
QY |||||
Db 1021 CCGTTTATCAGCAACGACAAAGCTGATTCGGTGTATTCGAGGCAACCA--- 1061
QY |||||
QY 1062 -----AAATAGCCCGCTGCGCTCTGGAACACACCAAAATCTTGT 1101
QY |||||
Db 1081 ACAGCAAGCGCATCAGATACAAATCTGCGCTGCGCTCTGGAACACACCAAAATCTTGT 1140
QY |||||
QY 1102 GATTTCTGAAATTTCCGTTGATGAGGCAAGTGTGAAATCCCGGACCGTTTGCAT 1161
QY |||||
Db 1141 GATTTCTGAAATTTCCGTTGATGAGGCAAGTGTGAAATCCCGGACCGTTTGCAT 1200
QY |||||
QY 1162 TCTCTATGCGGATTTTGGTCAATCCGCAAACTTCTTGTGGAAGGCGATGAAATTCCT 1221
QY |||||

```
Db 1201 TCCACTATGCCCGATTTTGGTGTATCCCGACAACTTCTTGTGCGAAGGCGTGAATTCCT 1260
Qy 1222 TTGTTAGCCGAAGAAACCATCGAGCTTCCGACGGCAGGAAATGACCGTCAGTGCT 1281
Db 1261 TTGTTAAACCAAGAACCAACCATCGATCTTCCGACGGCAGGAAATGACCGTCGCTGCT 1320
Qy 1282 TGTTCGCACTTTTGAACCTATGTGAACCTCGGACGATATAAAACCGAACGCCCGCGCC 1341
Db 1321 TGTTCGCACTTTTGAACCTATGTGAACCTCGGACGATATAAAACCGAACGCCCGCGCTG 1380
Qy 1342 AAACCGAAGGCGCA-----GGACGAAGAGGATTCGGACATTTGATATAATGGGAA 1389
Db 1381 CAACCGAAGGCGCAGGATGAAGAGGGGACGACGAGGGGTGTAGCGGTGATTAACCGTAAA 1440
Qy 1390 GAAAGCGAAGCGAAATCGGCGATGAAGAGAGGCCACCGAAGATGACGCCGCGAGGAT 1449
Db 1441 GAAAGCGAAGCGAAATCGGCGATGAAGAGAGGCCACCGGAGACGAAGTCTGTAGAAGATGAA 1500
Qy 1450 GAAGCGCAGCGAAGAGCGAAGCCACAGAAAACGAAGACGCGGAGGAAGACGACGCTGAA 1509
Db 1501 GACGAAGATGAAGACGAAGAGAAATCGAAGAGAACTGAAGAGAGAGCTGAAGAGAA 1560
Qy 1510 GAACCTGAAGAGAAATCGTCGCC---AGAAGGCAACGGCAGTTCAAACGCCATCCTGCT 1566
Db 1561 GAACCGGAAGAAATTCGCGCGCAGAGAAAGGCAAGGCGGTTCAGGCAGCATCCTGCCC 1620
Qy 1567 GTCCCGGAAGCTCTAAAGGCGAGGATATCGACCTTTTCCTGAAAGGTATCCGACGGCA 1626
Db 1621 ACTCCGAAGCTCTAAAGGCGAGGACATCGACCTTTTCCTGAAAGGTATCCGACGGCG 1680
Qy 1627 GAAACGAATATTCGCAAACTGGAGAACGACGCTATACCGGCATCTGGGAAGCGGTATC 1686
Db 1681 GAACCGGACATCCAAAAAACGGAACGCGCGGATATACCGGCATCTGGGAAGCGGTATC 1740
Qy 1687 GGC-----AAACCCATTCAATGGGACAAATCATGCGGATTAAGAAAGCGGCA 1731
Db 1741 GGCCTATCGGATAGTGGTACGTCCATTCAAAGGATAGCTATGCG---AATCAAGGGGCA 1797
Qy 1732 AAACGATATTTACGTTGATTTTCGGCAAGAAATCGATTTTCGGACGCTGACGGAGAA 1791
Db 1798 AAAGCAGAAATTTACCGTTGATTTTGAAGCGAAGACGGTGTCCGGATCTGACAGAAAA 1857
Qy 1792 AACCGTGPAGAACCTGCTTTCCGTATTGAAAACGGCGGTGATTGAGGGCAACGGTTTCAT 1851
Db 1858 AATGATACAAACCCCGCTTTTATTTGAAAAGGTGATGACGGTAAACGGTTTCAC 1917
Qy 1852 CGCAGCGCGCACTCGGATGACGGCATCGACCTTTCCGGCGAGGGTTGACACCAAAACG 1911
Db 1918 GCTTTGGCGCATACTCGGGAGAACGGTATTGACCTTTCTGGCGCAGGGTTGCACTAACCCG 1977
Qy 1912 CAGATCTCAAGCTAATGATCTTCGTGTAAGAGGATTTTACGGCCCGAGCGGAG 1971
Db 1978 AAGAACTTCAAGCGGCAATCTTCTTGTAAACGGCGCTTTTATGGCCCGAGCGGCA 2037
Qy 1972 GAATTGGCGGTATTATTTTCAATAATGATGGAAATCTCTTGTGATATACTGAAGGTACT 2031
Db 2038 GAATTGGCGGTATTATTTATCGACAGCACCGGAAATTCGGTTCGGGTATTTGGGCGGAA 2097
Qy 2032 GAAATAAAGTTGAAGC 2048
Db 2098 AAAGATGACAAGGAGC 2114
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RESULT 7

US-10-343-561-15

; Sequence 15, Application US/10343561

; Publication No. US20040126389A1

; GENERAL INFORMATION:

; APPLICANT: Berthet, Francois-Xavier Jacques

; APPLICANT: Dalemans, Wilfried

; APPLICANT: Denoel, Philippe

; APPLICANT: Dequesne, Guy

; APPLICANT: Feron, Christiane

```
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thonnard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343,561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15
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Query Match 31.2%; Score 678.6; DB 17; Length 1000;

Best Local Similarity 82.4%; Pred. No. 6.3e-151; Indels 13; Gaps 4;

Matches 830; Conservative 0; Mismatches 164;

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Qy 1174 GATTTTGGTCATCCCGCAAACTTCTTGTGCGAAGGCGATGAAATTCCTTTGGTTAGCCAA 1233
Db 1 GATTTTGGTCATCCCGCAAACTTCTTGTGCGAAGGCGTGAATTCCTTTGGTTAGCCAA 60
```

```
Qy 1234 GAGAAAACCATCGAGCTTCCGACGGCAGGAAATGACCGTCAGTCTTGTTCGACTTT 1293
Db 61 GAGAAAACCATCAAGCTTCCGATGGCAGGAAATGACCGTCCGTGCTTGTTCGACTTT 120
```

```
Qy 1294 TTGACCTATGTGAAACTCGGACGATATAAAACCGAACCCCGCGCCAAACCGAAGCG 1353
Db 121 TTGACCTATGTGAAACTCGGACGATATAAAACCGAACCCCGCGCAAGTAACCAAGCG 180
```

```
Qy 1354 CAGGACGAA---GAGGATTCGGACATTTGATATCGCGAAGAAAGCGAAGCAATCGGC 1410
Db 181 GAAGATAAAGGGAGGATGAAGAGATGTCAGGCGTTGTTAACTCGAAGAAGGCGAAGGC 240
```

```
Qy 1411 GATGAGNAGAGAGGACCGAAGATGCAGCCGACGAGATGAGCGCAGGAGAGAGACGAA 1470
Db 241 GAACTTTCCGAAGATGAAGGCGAAGAACCGAAGAAATCGTGAAGAAAGACCCGAAGAA 300
```

```
Qy 1471 GCCACAGAAAACGAAGCGGCGAAGACGAAAGCTGAAGAACCTGAAGAAAGAAATCGTCG 1530
Db 301 GAAGCTGAGAGGAGAGAGCTGAACCCGAAAGAGTTGAAGAAACCGAAGAAATTCGCG 360
```

```
Qy 1531 GCAGAAGGCAACGGCA---GTTCAACGCCATCTCTGCTGTCGCGAAGCTCTTAAAGC 1587
Db 361 ACAGAAGAAGCGGACAGCGTTCAAACGCCATCTCTGCTGCTCGAAGACCTCTAAAGC 420
```

```
Qy 1588 AGGATATCGACCTTTTCTGAAAGTATCGGACGGCAGAAACGAATATTCGCAAACT 1647
Db 421 AGGACATCGACCTTTTCTGAAAGTATCGGCGAAGCGGACATTCCTCAAGAAC 480
```

```
Qy 1648 GGAGAGCACCTATACCGCATTTGGGAGCGGTATCGGCAAAACCCATTCATTCGAGC 1707
Db 481 GGAAAGCACACTATACCGCATTTGGGAGCGGTATCGGCAACCCATTCATTCGAGC 540
```

```
Qy 1708 AATCATCGGATAAAGAGCGGCAAAAGCAGTATTTACCGTTGATTTTCGGAAGAAATCG 1767
Db 541 AATCAGCGCGATAAAGAGCGGCAAAAGCAGAAATTTACCGTTAATTTTCGCGAGAAATCG 600
```

```
Qy 1768 ATTTCCGGAACGCTGACGGAGAAAAAACGGTGTAGAACCTGCTTCCGTTATTTGAAACGGC 1827
Db 601 ATTTCCGGAACGCTGACGGAGAAAAAACGGTGTAGAACCTGCTTCTATATTTGAAACGGC 660
```

```
QY 1828 GTGATTGAGGGCAACGGTTTCATGCGACGCGCACTCGGGATGACGCAATCGACCTT 1887
Db 661 AAGATTGAGGGCAACGGTTTCATGCGCAACAGCAGCACTCGTGAGAACGGCATCAATCTT 720
QY 1888 TCGGGCGAGGTTTCGACCAACCGCAGATCTTCAAGCTAATGATCTTCTGTAGAGCA 1947
Db 721 TCGGGAATGGTTTCGACCAACCCAGAACCTTCCAAGCTAGTGATCTTCTGTAGAGGA 780
QY 1948 GGATTTTACGGCCGAGGCGGAGGAATTGGCGGTATTAATTTCAATAATGATGGAAA 2007
Db 781 GGATTTTACGGCCGCA-CGGAGGAATTGGCGGTATTAATTTCAATAAGATGGAAA 839
QY 2008 TCTCTTGGTATACTGAAGTACTGAAATAAAGTTGAAGTGAAGTGAAGTTGATGT 2067
Db 840 TCTCTTGGTATACTGAAGTACTGAAATAAAGTTGAAGTGAAGTGAAGTTGATGT 899
QY 2068 GATGTTGATGTTGATCTGATCTGATGTTGACAGTTAAACCTGAAGTTAAACCCCA 2127
Db 900 GAAGCTGAACCTGGTGTGTCGAACAGTTAGAAC-----CTGATGAAGTTAAACCCCA 953
QY 2128 TTCGGCGTGTATTCGGTTCGGAAGAAAGATAATAAAGAGTGGAAA 2174
Db 954 TTCGGCGTGTATTCGGTTCGGAAGAAAGATAATAAAGAGTGGAAA 1000

RESULT 8
US-10-467-534-80
; Sequence 80, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verilant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-80

Query Match 8.0%; Score 174.2; DB 17; Length 3300;
Best Local Similarity 77.2%; Pred. No. 1.4e-30;
Matches 240; Conservative 0; Mismatches 38; Indels 33; Gaps 1;

QY 1865 CTCGGGATACGGCATCGACCTTCGGCGAGGTTCCGACCAACCGCAGATCTTCAAG 1924
Db 1 CTCGGGATACGGCATCAATCTTCGGGAATGGTTGCACTAATCTCTCAAGTTTCAAAG 60
QY 1925 CTAATGATCTTCGTGTAGAAGGAGGATTTTACGGCCCGAGGAGGAATTTGGCGGTA 1984
Db 61 CCGACAATCTTCTGTACGGCGGCTTTTACGGCCCGAGGCGGAGNATTTGGCGGCA 120
QY 1985 TTATTTTCAATGATGGGAATCTTTGGTATTAATCTGAAGTACTGAAATAAAGTTG 2044
Db 121 CTAATTTCAATGATGGGAATCTTTGGTATTAATCTGAAGTACTGAAATAAAGTTG 180
QY 2045 AAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2104
Db 181 AATATGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 207
QY 2105 TAAACCTGAAGTTAAACCCCAATTCGGCGTGTATTCGGTTCGGAAGAAAGATAAAG 2164
Db 208 TAGAACCTGAAGTTAAACCCCAATTCGGCGTGTATTCGGTTCGGAAGAAAGATAAAG 267
```

```
QY 2165 AGGTGGA AAA 2175
Db 268 AGGTGGA AAA 278
```

RESULT 9

US-10-087-192-463/c

```
; Sequence 463, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 31124
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31124)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-463
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Query Match 3.8%; Score 81.6; DB 13; Length 31124;

Best Local Similarity 61.1%; Pred. No. 5.8e-08;

Matches 132; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

```
QY 1322 AAACCGAACGCCCGCCCAACCGAAGCGCAGGACGAGGATTCGGACATTGATA 1381
Db 18612 AAAAAGAAAAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18553
```

```
QY 1382 ATGGCGAAGAACCGAAGACGAAATTCGGCGATGAGAAGACCGACCGGATGCGCGG 1441
Db 18552 AAGAAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18493
```

```
QY 1442 CAGGAGATGAAGCGCAGAGAGAGACGAGCCACAGAAACGAGACCGCGGAGAGACG 1501
Db 18492 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18433
```

```
QY 1502 AAGCTGAAGAACCTGAAGAAGAAATCGTCGGCAGAAAG 1537
Db 18432 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 18397
```

RESULT 10

US-10-087-192-1627/c

; Sequence 1627, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSeq for Windows Version 4.0


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US-10-027-632-269927/c
; Sequence 269927, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269927
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-269927

Query Match          3.6%; Score 78.2; DB 16; Length 635;
Best Local Similarity 63.0%; Pred. No. 3.9e-08;
Matches 119; Conservative 1; Mismatches 69; Indels 0; Gaps 0;

QY 1349 AGCGCAGCAGCAGGAGGATTCGGACATTGATATCGCGAAGAAACGCGAAGCGAAATCG 1408
Db 452 AAGAGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393

QY 1409 GCGATGAGCAGCAGCAGCAGGAGGATTCGGACATTGATATCGCGAAGAAACGCGAAGCG 1468
Db 392 GAGAGGAGCAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 333

QY 1469 AAGCCACAGAAACCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1528
Db 332 AAGAAGCAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 273

QY 1529 CGCAGAG 1537
Db 272 AAGAAGAG 264

RESULT 14
US-09-864-761-19262/c
; Sequence 19262, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19262
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011416.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 35
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: P05156, EVALUE 9.40e+00
; OTHER INFORMATION: NT HIT: U67539.1, EVALUE 7.40e-01
; OTHER INFORMATION: EST_HUMAN HIT: BF129635.1, EVALUE 1.10e+00
US-09-864-761-19262

Query Match          3.6%; Score 78; DB 9; Length 305;
Best Local Similarity 63.2%; Pred. No. 2.8e-08;
Matches 120; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1347 GAAGCGCAGCAGCAGGAGGATTCGGACATTGATATCGCGAAGAAACGCGAAGCGAAAT 1406
Db 202 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 143

QY 1407 CGCGCATGAAGAAGAGGAGCAGCGAGATGCGCGCAGGAGATGAAGCGCAGCGAAGAGA 1466
Db 142 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 83

QY 1467 CGAGCCACAGAAACGAGAGCGCGAGAGACCGAGAGCTGAAGACCTGAAGAGAAATC 1526
Db 82 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 23

QY 1527 GTCGGCAGAA 1536
Db 22 ATTAAAGNA 13
```


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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 19:47:16 ; Search time 782 Seconds

(without alignments)
8819.139 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175

Sequence: 1 atgtgtaaacgcaattatgg.....ataataaagagggtggaaaaa 2175

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5669501 seqs, 1585417693 residues

Total number of hits satisfying chosen parameters: 11339002

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New:*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
- 9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	80	3.7	601	5	US-09-949-003C-61279	Sequence 61279, A
c 2	79.6	3.7	40778	5	US-09-949-003C-4003	Sequence 4003, Ap
c 3	79.6	3.7	40779	5	US-09-949-003C-5256	Sequence 5256, Ap
4	79	3.6	379	1	PCT-US02-39555A-2260	Sequence 2260, Ap
5	77.4	3.6	336	7	US-10-674-124A-14888	Sequence 14888, A
6	76.4	3.5	472	7	US-10-674-124A-5858	Sequence 5858, Ap
7	76.4	3.5	104595	7	US-10-796-307-8719	Sequence 8719, Ap
8	75.8	3.5	105046	5	US-09-949-003C-4057	Sequence 4057, Ap
9	75.8	3.5	105046	6	US-10-896-891-562	Sequence 562, App
10	75.4	3.5	450000	7	US-10-650-449A-3	Sequence 3, Appli
c 11	74.2	3.4	6074	6	US-10-896-164-12927	Sequence 12927, A
c 12	74.2	3.4	6074	8	US-10-868-184A-12927	Sequence 12927, A
c 13	74.2	3.4	6074	8	US-10-868-184-12927	Sequence 12927, A
c 14	73.4	3.4	186191	1	PCT-US04-02652-10794	Sequence 10794, A
c 15	73.4	3.4	186191	7	US-10-767-471-10794	Sequence 10794, A
16	72.2	3.3	195909	5	US-09-949-003C-3723	Sequence 3723, Ap
17	72.2	3.3	195910	5	US-09-949-003C-5418	Sequence 5418, Ap
c 18	72	3.3	392	7	US-10-674-124A-155	Sequence 155, App
19	71.6	3.3	447	7	US-10-674-124A-6601	Sequence 6601, Ap
20	71.6	3.3	573	7	US-10-674-124A-20334	Sequence 20334, A
21	71.6	3.3	678	1	PCT-US04-12047-412	Sequence 412, App
22	71.4	3.3	8917	5	US-09-404-520B-2417	Sequence 2417, Ap
c 23	71.4	3.3	1091282	6	US-10-915-727-12218	Sequence 12218, A
24	71	3.3	840	1	PCT-US04-12047-111	Sequence 111, App

25	71	3.3	2232	7	US-10-808-727-45	Sequence 45, Appl
c 26	71	3.3	263852	7	US-10-812-232-6	Sequence 6, Appli
c 27	71	3.3	816609	9	US-60-550-051-2987	Sequence 2987, Ap
28	70.6	3.2	213541	9	US-60-592-408-149	Sequence 149, App
c 29	70.2	3.2	28037	7	US-10-796-307-8704	Sequence 8704, Ap
30	69.4	3.2	17088	1	PCT-US04-02652-10707	Sequence 10707, A
c 31	69.4	3.2	17088	7	US-10-767-471-10707	Sequence 10707, A
c 32	69.4	3.2	34403	1	PCT-US04-02652-10620	Sequence 10620, A
c 33	69.4	3.2	34403	7	US-10-767-471-10620	Sequence 10620, A
c 34	69.2	3.2	41386	9	US-60-582-609-19329	Sequence 19329, A
c 35	69	3.2	27950	9	PCT-US04-11912-5	Sequence 5, Appli
36	68.6	3.2	549	1	PCT-US04-12049-5	Sequence 12217, A
37	68.6	3.2	549	1	PCT-US04-12049-5	Sequence 5616, Ap
c 38	68.6	3.2	510510	7	US-10-796-280-12217	Sequence 23154, A
c 39	68.6	3.2	510510	9	US-60-548-091-5616	Sequence 437, App
c 40	68.4	3.1	386	7	US-10-674-124A-23154	Sequence 5330, Ap
c 41	68.4	3.1	173354	9	US-60-592-408-437	Sequence 5649, Ap
c 42	68.2	3.1	268	7	US-10-674-124A-5330	Sequence 568, App
43	68	3.1	457	7	US-10-674-124A-5649	Sequence 363, App
c 44	67.6	3.1	148834	9	US-60-592-408-568	
45	67.4	3.1	1437	1	PCT-US04-12047-363	

ALIGNMENTS

RESULT 1
US-09-949-003C-61279
; Sequence 61279, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC DISORDERS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 61279
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-003C-61279

Query Match 3.7%; Score 80; DB 5; Length 601;
Best Local Similarity 62.9%; Pred. No. 7.5e-10;
Matches 122; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY	1348	AAGCGCAGGACGAGAGGATTCGACATTGATATGCGGAGAGAGCGAGACGAATC	1407
DB	112	AAAGAAGAGGAA	171
QY	1408	GCGCATGTAAGAAGAGGACCGCAGGATGCGCGCAGGAGATGAAAGCGGAGAGAC	1467
DB	172	GAAGAA	231
QY	1468	GAAGCCACAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1527
DB	232	GAAGAAGAA	291
QY	1528	TCGCGAGAGAGGCAA	1541
DB	292	GAAGAAGAGAGAGAA	305

RESULT 2
US-09-949-003C-4003/c
; Sequence 4003, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC DISORDERS, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF

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; FILE REFERENCE: CL0000791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4003
; LENGTH: 40778
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-003C-4003

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Query Match	3.7%;	Score 79.6;	DB 5;	Length 40778;
Best Local Similarity	64.8%;	Pred. No. 6.4e-09;		
Matches 118; Conservative	0;	Mismatches 64;	Indels 0;	Gaps 0;
QY	1343	AACCGAGGGCCGAGGAGGATTTCGCACATTTGTAATCGCGAAGAAGCGAAGACG	1402	
Db	22601	AAGAGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	22542	
QY	1403	AAATCGCGGATGAAGAAGAGGCCGACGAGATGCTGCACCAGAGATGAAGCAGCGAAG	1462	
Db	22541	AAGAAGAAGAAG	22482	
QY	1463	AAGACAGAGCCACAGAAAAACGAGAGCGGCGAGAGAGACGAAGCTCAAGAACCTGNAAGAG	1522	
Db	22481	AAGAAG	22422	
QY	1523	AA 1524		
Db	22421	AA 22420		

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RESULT 3
US-09-949-003C-5256/c
; Sequence 5256, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO00791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5256
; LENGTH: 40779
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-003C-5256

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[illegible]

Db 22421 AA 22420

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RESULT 4
PCT-US02-39555A-2260
; Sequence 2260, Application PC/TUS0239555A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Ghosh, Malabika
; APPLICANT: Xue, Aidong J.
; APPLICANT: Asundi Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Dunrui
; APPLICANT: Goodrich, Kyle W.
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Gezhi
; APPLICANT: Xu, Chongjun
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 820/PCT
; CURRENT APPLICATION NUMBER: PCT/US02/39555A
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/339,739
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 10/128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/365,384
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/365,091
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/372,615
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/376,045
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/372,381
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; Remaining Prior Application data removed -
; NUMBER OF SEQ ID NOS: 3134
; SOFTWARE: pc_FL_genes Version 6.0
; SEQ ID NO 2260
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US02-39555A-2260

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	Query Match	3.6%	Score 79;	DB 1;	Length 379;	
	Best Local Similarity	64.5%;	Pred. No. 1.1e-09;			
	Matches 118;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;	
QY	1355	AGGACGAAGAGATTTCGGACATTTGATTAATGGCCGAAGAAGCGAAGACGAANTCGGCATG	1414			
Db	169	AAGAAGAAGAAGAAAGAGAGAGAAGAAGACAAGAGAAGAAGAAGAGTAGTAGGAGAAG	228			
QY	1415	AAGAAGAAGGCCCGCAAGATCGAGCCGAGGAGATCATGGCAGCAAGAGACGAAGCCA	1474			
Db	229	GAGAAGGGAAGGAGAAGGAGAGAAGAAGAGAGAGAGGAGGAGAGAAGAAGAAGAAG	288			
QY	1475	CAGAAAACGAAGACGGCGAAGAACGCAAGCTCAAGAACTCTGAAGAGAAGATCTCTGGCAG	1534			


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; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12927
; LENGTH: 6074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-896-164-12927

Query Match      3.4%; Score 74.2; DB 6; Length 6074;
Best Local Similarity 65.8%; Pred. No. 6.2e-08;
Matches 123; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 1342 AAACCGAAGCGCAGACGAGAGGATTTCGGACATTGTGATTAATGCGGAGAAACCGAGAC 1401
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Db 2767 AAGGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2709

QY 1402 GAAATCGCGCATGAAGAAGAGCCACCGAAGATGCGAGCGCGAGAGATGAAGCGCGAA 1461
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Db 2708 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2649

QY 1462 GAAGACGAAGCCACAGAAACGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2648 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2589

QY 1522 GAATCGT 1528
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Db 2588 AATCTCT 2582
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RESULT 12
US-10-868-184A-12927/c
; Sequence 12927, Application US/10868184A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184A
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2000-03-09
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12927
; LENGTH: 6074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-896-164-12927

Query Match      3.4%; Score 74.2; DB 8; Length 6074;
Best Local Similarity 65.8%; Pred. No. 6.2e-08;
Matches 123; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 1342 AAACCGAAGCGCAGACGAGAGGATTTCGGACATTGTGATTAATGCGGAGAAACCGAGAC 1401
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Db 2767 AAGGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2709

QY 1402 GAAATCGCGCATGAAGAAGAGCCACCGAAGATGCGAGCGCGAGAGATGAAGCGCGAA 1461
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Db 2708 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2649

QY 1462 GAAGACGAAGCCACAGAAACGAGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
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Db 2648 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2589

QY 1522 GAATCGT 1528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2588 AATCTCT 2582
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 19:20:32 ; Search time 5538 Seconds
(without alignments)
11728.104 Million cell updates/sec

Title: US-10-735-098-1_COPY_100_2274

Perfect score: 2175
Sequence: 1 atgtgtaaacggaattatgg.....ataataaagggtggaaaaa 2175

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: em_estin:*
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14: gb_est5:*
15: em_estfun:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	83.8	3.9	289	14	CA716220 wdk3c.pk0
C 2	82.8	3.8	754	12	BI454583
C 3	82.2	3.8	739	28	BZ220379
C 4	82	3.8	675	28	BZ104011 CH230-227

5	81.6	3.8	531	14	CD915362
6	81.6	3.8	744	28	BH054422
C 7	81.4	3.7	355	29	CE349803
C 8	81.4	3.7	434	14	CA745444
C 9	81.2	3.7	265	14	CA607797
C 10	81.2	3.7	719	28	BH360392
C 11	81	3.7	263	13	BU005139
C 12	80.8	3.7	729	29	CE180020
C 13	80.6	3.7	264	13	BQ241566
C 14	80.6	3.7	501	12	BI504790
C 15	80.6	3.7	527	28	AZ279446
C 16	80.4	3.7	960	28	CE143364
C 17	80.2	3.7	799	28	BZ201507
C 18	80.2	3.7	880	28	AZ529191
C 19	80.2	3.7	1096	14	CK206118
C 20	79.6	3.7	341	29	CE510654
C 21	79.6	3.7	551	12	BM650535
C 22	79.4	3.7	540	28	AZ813205
C 23	79.4	3.7	665	13	BU432980
C 24	79.2	3.6	477	14	CD311846
C 25	79.2	3.6	575	10	BF707975
C 26	79	3.6	205	13	BQ241058
C 27	79	3.6	232	29	CG321416
C 28	79	3.6	301	29	CE339332
C 29	79	3.6	546	28	AZ600777
C 30	79	3.6	558	28	BH346798
C 31	79	3.6	596	29	CC660549
C 32	78.6	3.6	421	28	AZ113646
C 33	78.6	3.6	816	28	AZ535744
C 34	78.6	3.6	924	13	BQ925195
C 35	78.4	3.6	395	29	CE760553
C 36	78.4	3.6	605	28	BZ222147
C 37	78.2	3.6	638	12	BJ461550
C 38	78.2	3.6	617	14	CA743799
C 39	78	3.6	617	14	CA743799
C 40	77.8	3.6	223	13	CA022136
C 41	77.8	3.6	538	28	AZ825077
C 42	77.8	3.6	585	28	AZ564151
C 43	77.8	3.6	613	29	CE357285
C 44	77.6	3.6	504	29	CG354005
C 45	77.6	3.6	871	29	CG354013

ALIGNMENTS

RESULT 1	CA716220	289 bp	mRNA	linear	EST 26-NOV-2002
CA716220/c	wdk3c.pk024.122	wdk3c	Triticum aestivum	cdna	clone wdk3c.pk024.122
LOCUS	5' end	mRNA sequence.			
DEFINITION	CA716220	GI:25438013			
ACCESSION	CA716220.1				
VERSION	EST.				
KEYWORDS	Triticum aestivum (bread wheat)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
ORGANISM	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Poideae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 289)				
AUTHORS	Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,				
	Miao, G., Caraher, N. and Hanafey, M.K.				
TITLE	DuPont Wheat cDNA Sequence				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Scott V. Tingey				
	Crop Genetics				
	E. I. DuPont de Nemours and Company				
	1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA				
	Tel: 302-631-2602				
	Fax: 302-631-2607				
	Email: Scott.V.Tingey@USA.dupont.com				
	Seq primer: M13.				
FEATURES	Location/Qualifiers				

/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

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ORIGIN
Query Match      3.8%; Score 82.2; DB 28; Length 739;
Best Local Similarity 64.4%; Pred. No. 2e-05;
Matches 123; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1347 GAAGGCGCAGGACGAAGAGGATTGCGACATTGATATGCGGAAGAAAGCGAAGC 1406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 663 GAAGAGGAAGAGGAGGAGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 604

QY 1407 CGGCGATGAAGAGAGCGCCGAGAGTGCAGCCGCGAGGAGATGAAGCGCAGGAGAA 1466
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 603 AGAAGAAGAAAGAAAGAAAGAAAGAGGAGGAAGAAAGAGGAGGAAGAAAGAA 544

QY 1467 CGAGGCCACAGAAACGAGACGCGGAGAGAGACGAGCTGAAGAACTGAAGAGAAATC 1526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 543 AGAAGAGCAGAGAAAGAGCAGAGAAAGAAAGCAGAGAGCAGAGAGAGAGCAGA 484

QY 1527 GTCGCGCAGAAG 1537
      |||||
Db 483 AGAGCAGAG 473

```

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RESULT 4
LOCUS BZ104011
DEFINITION CH230-227F5.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
          675 bp DNA linear GSS 10-OCT-2002
VERSION CH230-227F5, Genomic survey sequence.
ACCESSION BZ104011
VERSION BZ104011.1 GI:23744890
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 675)
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
          Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
          Riggs, F., de Jong, P., and Fraser, C.M.
          Rat BAC End Sequences from Library CHORI-230 EcoRI segment
          Unpublished (1999)
          Other GSSs: CH230-227F5.TV
          Contact: Shaving Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the rat BAC library CHORI-230
          (http://www.chori.org/bacpac/rat230.htm). For BAC library
          availability, please contact Pieter de Jong (pjejong@mail.cho.org).
          Clones may be purchased from BACPAC Resources
          (http://www.chori.org/bacpac/or ering information.htm). BAC end
          page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
          Plate: 227 row: F column: 5
          Seq primer: SP6
          Class: BAC ends.
FEATURES
          source
            1..675
              /organism="Rattus norvegicus"
              /mol_type="genomic DNA"
              /strain="BN/SSNHsd/MCW"
              /db_xref="taxon:10116"
              /clone="CH230-227F5"
              /sex="Female"
              /cell_type="Brain"
              /clone_lib="CHORI-230 Segment 1"
              /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;

```

CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

```

ORIGIN
Query Match      3.8%; Score 82; DB 28; Length 675;
Best Local Similarity 61.9%; Pred. No. 2.2e-05;
Matches 130; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1343 AACCGAGGCGCAGGACGAAGAGGATTGCGACATTGATATGCGGAAGAAAGCGAAGC 1402
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 325 AAGAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 384

QY 1403 AAATCGCGCGATGAAGAGAGAGCCAGCAGATGCGAGCCGCGAGGAGATGAAGGGCGCAG 1462
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 385 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444

QY 1463 AAGAGAGAGCCACAGAAACAGAGACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1522
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 504

QY 1523 AATCGTCGCGCAGAGGCAACCGCGAGTTCAA 1552
      |||||
Db 505 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534

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RESULT 5
LOCUS CD915362
DEFINITION G550.125001F010713 G550 Triticum aestivum cDNA clone G550125001,
          mRNA sequence.
ACCESSION CD915362
VERSION CD915362.1 GI:32689686
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Pooidae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 531)
AUTHORS Genoplante.
          Genoplante, a major partnership french program in plant genomics
          Unpublished (2003)
          Contact: Genoplante
          Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.inbio.fr).
FEATURES
          source
            1..531
              /organism="Triticum aestivum"
              /mol_type="mRNA"
              /cultivar="recital"
              /db_xref="taxon:4565"
              /clone="G550125001"
              /tissue_type="grain (550 degrees per day after
              pollination)"
              /clone_lib="G550"

```

```

ORIGIN
Query Match      3.8%; Score 81.6; DB 14; Length 531;
Best Local Similarity 61.1%; Pred. No. 2.6e-05;
Matches 132; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1329 ACGCCCGCGCGCAACCGAGCGCAGGACGAGAGAGGATTCGGACATTGATTAATGGCGA 1388
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 ACGCGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62

QY 1389 AGAAAGCGGAGAGACGAAATCGGCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122

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[illegible]

RESULT	6
LOCUS	BH065422
DEFINITION	744 bp DNA linear GSS 18-JUL-2001 RPCI-24-296J10.TV RPCI-24 Mus musculus genomic clone
ACCESSION	BH065422
VERSION	BH065422
KEYWORDS	BH065422.1 GI:11482369
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumariota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 744)
AUTHORS	Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tseday,G., Geer,K., Krol,M., Shvartsbeyn,A., Gabregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
TITLE	Mouse PAC End Sequences from Library RPCI-24
JOURNAL	Unpublished (1999)
COMMENT	Other_GSSs: RPCI-24-296J10.TV

Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cno.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 296 row: J column: 10
Seq primer: SP6
Class: BAC ends.

```

FEATURES
source
Class: BAC clus.
Location/Qualifiers
1. .744
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-296J10"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/notes="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."
ORIGIN

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Query Match 3.8%; Score 81.6; DB 28; Length 744;
Best Local Similarity 62.0%; Pred. No. 2.7e-05;
Matches 129; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

1342	AAACCGAAGCCGAGAGCGAAGAGGATTCCGACATTGATTAATGCGCAAGAAAGCGCAAGAC	1401
166	AAGAAGAGGAGGAGGAGGAGAGGAGAAAGATCGAAGGAAGAAGAGGAGGAAGAAGAG	225
1402	GAATCGGCGATGAAGAAGAAGCACCAGATGTCGCGCCGAGAGATGAAGCGACGCAA	1461
226	GAAGGAGGAGAAAGAAAGAGGAGGAGGAGGAGAGGAGGAAGAAGAGGAGGAAGAGCAA	2295

[illegible]

RESULT 7	
CE349803/c	
LOCUS	CE349803 355 bp DNA linear GSS 26-SEP-2003
DEFINITION	tigr-gss-dog-17000334166020 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION	CE349803
VERSION	CE349803.1
KEYWORDS	GI:36183437
SOURCE	GSS.
ORGANISM	Canis familiaris (dog) Canis familiaris Fukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	1 (bases 1 to 355)
AUTHORS	Kirkness,E.F.,Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE	The dog genome: survey sequencing and comparative analysis
JOURNAL	Science 301 (5641), 1898-1903 (2003)
MEDLINE	22875432
PUBMED	14512627
COMMENT	Contact: Kirkness EF

FEATURES source

ORIGIN

Query Match 3.7%; Score 81.4; DB 29; Length 355;
Best Local Similarity 55.0%; Pred. No. 2.8e-05;
Matches 160; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY	1262	GGAAAATGACCGTCAGTGTCTGTTGGCAGCTTTTGTGACCTTATGTGAAACTCGGACGGATAA	1321
Db	332	GA AAAATGAATATCTCTAAATTTTGAATCTATCTGTGGCTCTTGGGA CAATGGGCGATCAA	273
QY	1322	AAACCGAACCCCGCCGCCAAACCGAACCGCAGACGACGAGGAGATTCGGA CATTTGATA	1381
Db	272	GAAACAAAGAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG	213
QY	1382	ATGGCGGAAGAACGCGAAGACGAAATCGGCGATGAAGAAGAGGCCACCGAAGATGCGAGCCG	1441
Db	212	AAGAAGAAGAAGAAGAAGAAGAAAAGAAGAAGAAGAAGAAGAAGAAGAAG	153
QY	1442	CAGGAGATCAAGCGCAGGAAGAAGACGGAAGCCACAGAAACCGAGACGCGGAGAGACG	1501
Db	152	AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	93
QY	1502	AAGCTGAAGAACTTGAGAAGAATCGTCCGCGAAGCGCAACGGCAGTTCAA	1552
Db	92	AAGAAGAAGAAGAAGAAGAAGAAAAGAAGAGAGAGAGAGAGAGAGAGAGAAGA	12


```

RESULT 8
CA745444/c
LOCUS
DEFINITION
wri2s.pk001.i6 wri2s Triticum aestivum cDNA clone wri2s.pk001.i6 5'
end, mRNA sequence.
ACCESSION
CA745444
VERSION
CA745444.1 GI:25561267
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 434)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.tingey@USA.dupont.com
Seq primer: 17.
FEATURES
source
1..434
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri2s.pk001.i6"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="wri2s"
/note="Vector: pGEM-T Easy; Site 1: SmaI; Riband
(susceptible) wheat leaves infected with Septoria tritici
strain A, 48 hours after infection, subtracted w/
comparable uninfected leaves"
ORIGIN
Query Match 3.7%; Score 81.4; DB 14; Length 434;
Best Local Similarity 64.0%; Pred. No. 2.9e-05;
Matches 121; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1349 AGGCGCAGGACGAGAGGATTCGGACATTGTAATGGCGAAGACGGAATCG 1408
|||||
DB 360 AGGAGGACGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301
QY 1409 GCGNTGAGAGAGAGGACCGGAGATGCGCCGAGGAGATGAGCGGAGAGAGC 1468
|||||
DB 300 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
QY 1469 AAGCCACAGAAACGAGAGCGGCGAAGACGAGACGAGCTGAAGAACCTGCT 1528
|||||
DB 240 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 1529 CGGCGAAG 1537
|||||
DB 180 AAGAAGAG 172

RESULT 9
CA607797/c
LOCUS
DEFINITION
wri1.pk0082.f4 wri1 Triticum aestivum cDNA clone wri1.pk0082.f4 5'
end, mRNA sequence.
ACCESSION
CA607797
VERSION
CA607797.1 GI:25162959
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 265)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.tingey@USA.dupont.com
Seq primer: M13.
FEATURES
source
1..265
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri1.pk0082.f4"
/tissue_type="root"
/clone_lib="wri1"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) root; 7 day old
seedling, light grown"
ORIGIN
Query Match 3.7%; Score 81.2; DB 14; Length 265;
Best Local Similarity 64.1%; Pred. No. 3.1e-05;
Matches 116; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1357 GACGAGAGGATTCGGACATTGTAATGGCGAAGACGGAATCGCGATGAA 1416
|||||
DB 184 GATGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 125
QY 1417 GAAAGAGGACCGAGATGCGCGAGGAGATGAGGAGGAGAGAGAGAGAGAG 1476
|||||
DB 124 GAAAGAGAGAGAGAGAGAGATGANGAAGAGAGAGAGAGAGAGAGAGAGAA 65
QY 1477 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
|||||
DB 64 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 5
QY 1537 G 1537
4 G 4
DB 4 G 4

RESULT 10
BH360392
LOCUS
DEFINITION
CH230-107G3.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-107G3, genomic survey sequence.
ACCESSION
BH360392
VERSION
BH360392.1 GI:17291126
KEYWORDS
GSS.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 719)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-107G3.TU
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

```

Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived
 (<http://www.chori.org>)
 availability, please
 Clones may be purchased
 (<http://www.chori.org>)
 page: <http://www.tigr.org>
 Plate: 107 row: C
 Seq primer: T7
 Class: BAC ends.

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10
11. Feature 11	Source 11
12. Feature 12	Source 12
13. Feature 13	Source 13
14. Feature 14	Source 14
15. Feature 15	Source 15
16. Feature 16	Source 16
17. Feature 17	Source 17
18. Feature 18	Source 18
19. Feature 19	Source 19
20. Feature 20	Source 20
21. Feature 21	Source 21
22. Feature 22	Source 22
23. Feature 23	Source 23
24. Feature 24	Source 24
25. Feature 25	Source 25
26. Feature 26	Source 26
27. Feature 27	Source 27
28. Feature 28	Source 28
29. Feature 29	Source 29
30. Feature 30	Source 30
31. Feature 31	Source 31
32. Feature 32	Source 32
33. Feature 33	Source 33
34. Feature 34	Source 34
35. Feature 35	Source 35
36. Feature 36	Source 36
37. Feature 37	Source 37
38. Feature 38	Source 38
39. Feature 39	Source 39
40. Feature 40	Source 40
41. Feature 41	Source 41
42. Feature 42	Source 42
43. Feature 43	Source 43
44. Feature 44	Source 44
45. Feature 45	Source 45
46. Feature 46	Source 46
47. Feature 47	Source 47
48. Feature 48	Source 48
49. Feature 49	Source 49
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51. Feature 51	Source 51
52. Feature 52	Source 52
53. Feature 53	Source 53
54. Feature 54	Source 54
55. Feature 55	Source 55
56. Feature 56	Source 56
57. Feature 57	Source 57
58. Feature 58	Source 58
59. Feature 59	Source 59
60. Feature 60	Source 60
61. Feature 61	Source 61
62. Feature 62	Source 62
63. Feature 63	Source 63
64. Feature 64	Source 64
65. Feature 65	Source 65
66. Feature 66	Source 66
67. Feature 67	Source 67
68. Feature 68	Source 68
69. Feature 69	Source 69
70. Feature 70	Source 70
71. Feature 71	Source 71
72. Feature 72	Source 72
73. Feature 73	Source 73
74. Feature 74	Source 74
75. Feature 75	Source 75
76. Feature 76	Source 76
77. Feature 77	Source 77
78. Feature 78	Source 78
79. Feature 79	Source 79
80. Feature 80	Source 80
81. Feature 81	Source 81
82. Feature 82	Source 82
83. Feature 83	Source 83
84. Feature 84	Source 84
85. Feature 85	Source 85
86. Feature 86	Source 86
87. Feature 87	Source 87
88. Feature 88	Source 88
89. Feature 89	Source 89
90. Feature 90	Source 90
91. Feature 91	Source 91
92. Feature 92	Source 92
93. Feature 93	Source 93
94. Feature 94	Source 94
95. Feature 95	Source 95
96. Feature 96	Source 96
97. Feature 97	Source 97
98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

ORIGIN	Query Match	3.7%;	Score 81.2;	DB 28;	Length 719;
	Best Local Similarity	61.2%;	Pred. No. 3.2e-05;		
	Matches 131;	Conservative	0;	Mismatches 83;	Indels 0;
	Gaps	0;			
QY	1340	CCRAACCGAGGCGCAGACGAGAGGATTCGGACATTGATATGGCGAAGAACGGAAG	13999		
Db	229	CCCAATATGAGGAGGAGGAGGATGAGGAGATGAAGACGATGATGGCAATGAGGAAGAGG	288		
QY	1400	ACGAATTCGCGATGAAGAAGAGGCACCGAAGATGCAGCCGCGAGGAGATCAAGCGCG	14599		
Db	289	AGGAGGAGGAAGAGGAAGAGAGAAAGAGAAACGAATCGAAGCGAAGAGAAGAAGAAG	348		
QY	1460	AAGAAGACGAGCCACACGAANAACGAAGACGGCGNAGAGACGAAGCTGAAGACCTGAAG	1519		
Db	349	ACAAGAGAGAGAGAGAGAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAG	408		
QY	1520	AAGAATCTCGGCAGAGGCAACGGCAGTTCAAA	1553		
Db	409	AAAAAGAGAGGAAGACTGCAATTTTGTTCATA	442		

RESULT 11	
BU005139/c	
LOCUS	263 bp mRNA linear EST 22-AUG-2002
DEFINITION	QG7D20.Yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
ACCESSION	BU005139
VERSION	BU005139.1
KEYWORDS	GG7D20, mRNA sequence.
SOURCE	GI:22439534
ORGANISM	Lactuca sativa
	Lactuca sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichoriteae; Lactuca.
REFERENCE	1. (bases 1 to 263)
AUTHORS	Kozlak, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/

Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akorik@atcg.org [michelmore@vegmai-
singleton, see <http://cgpbp.ucdavis.edu/>]
Plate: QGG7 row: D column: 20.

FEATURES

ORIGIN	Query Match	3.7%; Score 81; DB 13; Length 263;
	Best Local Similarity 62.7%; Pred. No. 3.3e-05;	
	Matches 126; Conservative 0; Mismatches 75; Indels 0; Gaps 0;	
QY	1343 AACCGAAGCGCAGGACGAGACGATTCGGACATGTATATGGCGAGAAAGCCGAAGCG 1402	
Db	263 AACACAGACAAACAGAAAGAAAGAAAGAACGACGAAAGAAAGAAAGAAAGAAAG 204	
QY	1403 AAATCGCGCATGAAGAAAGAGCGCACCGAAGATGCGACGCGCAGGAGATGAAGCGCAGG 1462	
Db	203 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 144	
QY	1463 AAGACGAAGCCACAGAAACCGACAGCGCGCAGAGACGACGACTGTGAGAACCTTGAAGAAG 1522	
Db	143 AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 84	
QY	1523 AATCGTCGGCAGAAGGCAACG 1543	
Db	83 AAGACGAAGAAGAAAGACGAAG 63	

RESULT 12	
CE180020	729 bp DNA linear GSS 25-SEP-2003
LOCUS	tigr-gss-dog-17000326768259 Dog Library Canis familiaris genomic,
DEFINITION	genomic survey sequence.
ACCESSION	CE180020
VERSION	CE180020.1 GI:35328914
KEYWORDS	GSS.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS	Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE	The dog genome: survey sequencing and comparative analysis
JOURNAL	Science 301 (5641), 1898-1903 (2003)
MEDLINE	22875432
PUBMED	14512627
COMMENT	Contact: Kirkness EF

The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200

Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source

```

/crome-lib= boy library
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

```

ORIGIN

	Query Match	3.7%; Score 80.8; DB 29; Length 729;	
	Best Local Similarity 61.3%; Pred.No. 3.8e-05;		
	Matches 130; Conservative 0; Mismatches 82; Indels 0; Gaps 0;		
QY	1342	A A A C C G A A G C G C A G G A G A A G A G G A T T C G G A C A T T G A T T A T G C G A A G A A A A G C G A A C	1401
DB	172	A A G A A G N A G A G N A G N A G A G A G A G A A G A A G A A G A G A G A A G A A G A A G A A G A A	231
QY	1402	G A A A T C G G C G A T G A A G A A A A G G C A C C G A A G A T G T C A C C G C A G G A G A T G A A G C G A C G A A	1461
DB	232	G A A G A G A A G A A G A A G A A G A A A A A A G A A G A G A G A G A A G A A G A A G A A G A A G A A G A A	291
QY	1462	G A A G A A G A A G C C A G A A A A A A G A A G A G C G G C G A A G A A G A A C A A G C T G A A G A A C C T T G A A G A A	1521
DB	292	G A A G A G A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A G A A	351
QY	1522	G A A T C G T C G C A G A A G G C A A C G G C A G T T C A A A	1553
DB	352	G A G A A T T A G G A T C A A A A T A A T G A T T A A C A	383

RESULT 13	BQ241566	264 bp	mrna	linear	EST 03-MAY-2002
LOCUS	TaE05003E07R	TaE05	Triticum aestivum	cDNA clone	TaE05003E07R, mRNA
DEFINITION	BQ241566				
ACCESSION	BQ241566				
VERSION	BQ241566.1	GI:20437442			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.				
AUTHORS	1. (bases 1 to 264)				
TITLE	Cloutier,S.				
JOURNAL	Wheat functional genomics - Glenlea developing seeds cDNA libraries				
COMMENT	Unpublished (2002) Contact: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fax: (204) 983-4604 Email: scloutier@agr.gc.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb Plate: 003 row: E column: 07 Seg primer: M13 Reverse.				

FEATURES

source

```
/clone lib="TaE05"  
/note="vector: pSPORT-p (Invitrogen Technologies); Site_1:  
NotI; Site 2: MluI; mRNA obtained from wheat seeds of  
cultivar Glenlea 5 days post-anthesis"
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ORIGIN

Query Match	3.7%;	Score 80.6;	DB 13;	Length 264;
Best Local Similarity	65.0%;	Pred. No. 4e-05;		
Matches 119;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;
QY	1355	AGGACGAAGAGGATTCCGACATTTCATTAATGGCGAAGAAAGACGAAGACGAATAATCGCGCATG	1414	
Db	49	AACAAGAGAAGAGAGGAGAAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG	108	
QY	1415	AAGAAGAGCGCCGGAAGATGCAAGCCGACGAGAGATGAGCGACGGAAGAGACGAAGCCCA	1474	
Db	109	AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG	168	
QY	1475	CAGAAAACGAAGACGCGGAAGAAAGACGAAGACTCGAAGAACCTCGAAGAGAATAATCGTCGGCAG	1534	
Db	169	AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG	228	
QY	1535	AAG 1537		
Db	229	AAG 231		

RESULT 14	
BI504790	
LOCUS	501 bp mRNA linear EST 08-APR-2002
DEFINITION	BB170011A10D02.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170011A10D02 5', mRNA sequence.
ACCESSION	BI504790
VERSION	BI504790.1 GI:153555164
KEYWORDS	EST.
SOURCE	Apis mellifera (honeybee)
ORGANISM	Apis mellifera Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Apoidea; Apoidea; Apidae; Apis. 1 (bases 1 to 501) Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E. Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee Genome Res. 12 (4), 555-566 (2002) 21929762 11932240 Contact: Gene E. Robinson
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	
COMMENT	

FEATURES

Source

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/db xref="taxon:7460"
/clone="BB170011A10D02"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/notes="Organ: Brain; Vector: pT73-Pac; Site 1: EcoRI;
Site 2: NotI; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

```

ORIGIN

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Query Match      3.7%; Score 80.6; DB 12; Length 501;
Best Local Similarity 65.0%; Pred. No. 4.1e-05;
Matches 119; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1355 AGGACGAGAGGATTCGACATTGATGCGGAGAGAGCGAAGACGAAATCGCGATG 1414
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 59 AAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 118
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1415 AAGAAGAGCGACCGGAGATGCGCCGCGAGGATGAGGCGGAGAGAGACGAGCC 1474
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 119 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 178
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1475 CAGAAACGAGAGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1534
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 179 AAGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 238
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1535 AAG 1537
      |||||
Db 239 AAG 241

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RESULT 15

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AZ279446
LOCUS      AZ279446          527 bp    DNA    linear    GSS 26-JUL-2000
DEFINITION RPI-23-113H20.TJ RPI-23 Mus musculus genomic clone
            RPI-23-113H20, genomic survey sequence.
ACCESSION  AZ279446
VERSION    AZ279446.1 GI:9498348
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 527)
AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Megann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.W.
            Mouse BAC End Sequences from Library RPI-23
            Unpublished (1999)
            Other GSSs: RPI-23-113H20.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac/ends/mouse/bac\_end\_intro.html
            Plate: 113 row: H column: 20
            Seq Primer: SP6

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Class: BAC ends.

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FEATURES             Location/Qualifiers
     source            1..527
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPI-23-113H20"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
                     EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested
                     with a combination of EcoRI and EcoRI Methylase. Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI sites. The ligation products were transformed into
                     DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match      3.7%; Score 80.6; DB 28; Length 527;
Best Local Similarity 66.3%; Pred. No. 4.1e-05;
Matches 116; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1351 GCGCAGGACGAGAGGATTGCGACATTGTAATGCGGAGAGAAAGCGAAGATCGGC 1410
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 192 GAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 251
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1411 GATGAGAGAGAGGACCGAAGATGCGAGCGCGAGGAGATGAGGCGGAGAGAGAGAG 1470
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 252 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 311
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1471 GCCACAGAAAACGAGAGCGCGAGAGAGACGAGCTGAGAACCTGAGAGAGAGAT 1525
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 312 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 366

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Search completed: August 23, 2004, 23:38:24
Job time : 5543 secs